

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: STUYVER, LIEVEN  
ROSSAU, RUDI  
MAERTENS, GEERT
- (ii) TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
- (iii) NUMBER OF SEQUENCES: 313
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
  - (B) STREET: 1100 NORTH GLEBE ROAD
  - (C) CITY: ARLINGTON
  - (D) STATE: VIRGINIA
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 22201-4714
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/155,885
  - (B) FILING DATE: 08-OCT-1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/EP97/02002
  - (B) FILING DATE: 21-APR-1997
  - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: EP 96870053.4
  - (B) FILING DATE: 19-APR-1996
  - (C) CLASSIFICATION:
- (ix) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: SADOFF, B.J.
  - (B) REGISTRATION NUMBER: 36,663
  - (C) REFERENCE/DOCKET NUMBER: 2551-5
- (x) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703) 816-4000
  - (B) TELEFAX: (703) 816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGGTCACCAT ATTCTTGGG

19

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAACAAGAGC TACAGCATGG G

21

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCACTGCATG GCCTGAGGAT G

21

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GTTCCCKGAAC TGGAGCCACC AG

22

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TCTTTGTATT AGGAGGCTGT AG

22

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCTGTAGGCA TAAATTGGTC TG

22

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCCACAGWA GCTCCAAATT C

21

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GAAGGAAAGA AGTCAGAAGG C

21

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGGCTTTGGG GCATGG

16

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TGGCTTTAGG GCATGG

16

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGCTTTAGG ACATGG

16

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGTTGCATG GTGCTG

16

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CACCTCTGCC TAATCAT

17

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TGGGGTGGAG CCCTCAG

17

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCCAGCAGCC AACCAG

16

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCCATGGGGG ACTGT

15

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AACCCCAACA AGGATG

16

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TCCACCAGCA ATCCT

15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGGGGGAAGA ATATTT

16

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AAATTCCAGC AGTCCC

16

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GTTCCCAACC CTCTGG

16

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AACCTCGCAA AGGCAT

16

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TGCATTCAAA GCCAAC

16

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TACTCACAAC TGTGCC

16

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCCTGCGTT CGGAGC

16

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CAGGAAGACA GCCTAC

16

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GATCCAGCCT TCAGAG

16

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ATGCTCCAGC TCCTAC

16

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GCTTTCTTGG ACGGTC

16

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTACCCCAAT CACTCC

16

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AGCACCTCTC TCAACG

16

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CCAATGGCAA ACAAGG

16

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGAGGGCTC CACCCCA

17

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

ATCTCTTGTA CATGTC

16

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATCTCTTGTA CATGTC

16

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATCTCATGTT CATGTC

16

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CAGTGGGACA TGTACA

16

(2) INFORMATION FOR SEQ ID NO: 38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CAGTAGGACA TGAACA

16

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTTCAAGC CTCCAA

16

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AGCCTCCAAG CTGTGC

16

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

AAAGCCACCC AAGCA

16

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TGGCTTTAGG ACATGGA

17

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GACATGTACA AGAGATGA

18

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GACATGAACA TGAGATGA

18

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TGTACATGTC CCACTGTT

18

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TGTTTCATGTC CTACTGTT

18

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ACTGTTCAAG CCTCCAAG

18

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GGCACAGGCT TGGAGGCTT

19



(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AAAGCCACCC AAGGCACA

18

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CCCAGAGGGT TGGGAAC

17

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CAGCATGGGG CAGAATCT

18

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TCCACCAGCA ATCCTCTG

18

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGATCCAGCC TTCAGAGC

18

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TCAGGAAGAC AGCCTAC

17

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCAACCCCA ACAAGGATC

19

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AATGCTCCAG CTCCTAC

17

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CTGCATTCAA AGCCAACT

18

(2) INFORMATION FOR SEQ ID NO: 58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCCCATGGGG GACTGTTG

18

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CATACTCACA ACTGTGCCA

19

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GGGCTTTCTT GGACGGTCC

19

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CTCTCGAATG GGGGAAGA

18

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CCTACCCCAA TCACTCCA

18

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

AGCACCTCTC TCAACGACA

19

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCAAATTCCA GCAGTCCCG

19

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GCCAATGGCA AACAAAGTA

19

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GACATGAACA TGAGATG

17

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GGACATGAAC AAGAGAT

17

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GACATGTACA AGAGATG

17

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

ACATAAGAGG ACTCTTGGAC

20

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TACTTCAAAG ACTGTGTGTT TA

22

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ACAAAGACCT TTAAYCT

17

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ACAAAGATCA TTAAYCT

17

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TTCCACCAGC AATCCTC

17

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GATCCAGCCT TCAGAGC

17

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CAAGGTATGT TGCCCGTTTG TCC

23

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CCAAACAGTG GGGGAAAGCC C

21

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CTACGGATGG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

TACGGACGGA AACTGC

16

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 16 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TTCGGACGGA AACTGC

16

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

CTTCGGACGG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CTACGGATAG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CTTCGGACAG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTATGGGAGT GGCCTCAGY C

21

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GCTGTAGGCA TAAATTGGTC TG

22

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CTCCACAGWA GTCCTCAAATT C

21

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

ACATAAGAGG ACTCTTGGAC

20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TACTTCAAAG ACTGTGTGTT TA

22

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TAGGTAAAG GTCTTTGT

18

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TAGGTAAATG ATCTTTGT

18

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CATGTCCCAC TGTTCAC

17

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CATGTCCTAC TGTTCAC

17

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

TTCTGCCCCA TGCTGTA

17

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

TTCTGCCCCA TGCTGTAG

18

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GGTAWAAAGG GACTCAGAT G

21

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

TCAGCTATAT GGATGAT

17

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CAGCTATATG GATGAT

16

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TTCAGCTATA TGGATG

16

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TCAGTTATAT GGATGAT

17

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO



(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TTTCAGTTAT ATGGATG

17

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TTTAGTTATA TGGATGA

17

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TCAGCTATGT GGATGAT

17

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TCAGTTATGT GGATGAT

17

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTTCAGCTAT GTGGATG

17

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CAAGGTATGT TGCCCGTTTG TCC

23

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGYAWAAAGG GACTCAMGAT G

21

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GGGTCACCAT ATTCTTGGG

19

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GTTCCCKGAAC TGGAGCCACC AG

22

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CCGGAAAGCT TGAGCTCTTC TTTTTCACCT CTGCCTAATC

40

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CCGGAAAGCT TGAGCTCTTC AAAAAGTTGC ATGGTGCTGG

40

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

GTGGTTCGCC GGGCTTG

17

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CTGCGAGGCG AGGGAGTTCT TCTTC

25

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

TGCCATTTGT TCAGTGGTTC GTAGGGC

27

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

CCGGCAGATG AGAAGGCACA GACGG

25

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTCAGCTATA TGGATGAT

18

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

TCAGCTATAT GGATGATG

18

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TTCAGCTATG TGGATGAT

18

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TCAGCTATGT GGATGATG

18

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

GGCTTTGGGG CATGG

15

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TGGCTTTGGG GCATG

15

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GTGGCTTTGG GGCATG

16

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

GGCTTTGGGG CATGGA

16

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TGGCTTTGGG ACATGG

16

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

GGCTTTGGGA CATGG

15

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:



TGGCTTTGGG ACATG

15

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GTGGCTTTGG GACATG

16

(2) INFORMATION FOR SEQ ID NO: 126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GGCTTTGGGA CATGGA

16

(2) INFORMATION FOR SEQ ID NO: 127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

TCAGTTATAT GGATGATG

18

(2) INFORMATION FOR SEQ ID NO: 128:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

TTCAGTTATA TGGATGAT

18

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TTTCAGTTAT ATGGATGAT

19

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

TCAGTTATGT GGATGATG

18

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TTCAGTTATG TGGATGAT

18

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

TTTCAGTTAT GTGGATGAT

19

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TTTCAGTTAT GTGGATGA

18

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

TGCTGCTATG CCTCATCTTC

20

(2) INFORMATION FOR SEQ ID NO: 135:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CARAGACAAA AGAAAATTGG

20

(2) INFORMATION FOR SEQ ID NO: 136:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CTATGGATGG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CCTATGGATG GAAATTG

17

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

ACCTATGGAT GGAAATT

17

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CTCAAGGCAA CTCTATGTGG

20

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CTCAAGGCAA CTCTATGGG

19

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCAAGGCAAC TCTATGTTG

19

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATCCCATCAT CTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATCCCATCAT CTTGGGCGG

19

(2) INFORMATION FOR SEQ ID NO: 144:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

TCCCATCATC TTGGGCGG

18

(2) INFORMATION FOR SEQ ID NO: 145:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

CCCATCATCT TGGGCTGG

18

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

TTCGAAAAT ACCTATGG

18

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TTTCGCAAAA TACCTATG

18

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

CTTTCGCAAAA ATACCTATG

19

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TCGCAAAATA CCTATGGG

18

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TCTACTTCCA GGAACAT

17

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

TCTACTTCCA GGAACATC

18

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

CTCTACTTCC AGGAACAT

18

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

CTCTACTTCC AGGAACAG

18

(2) INFORMATION FOR SEQ ID NO: 154:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

CTGCACGATT CCTGCT

16

(2) INFORMATION FOR SEQ ID NO: 155:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

TGCACGATTC CTGCTCA

17

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

CTGCACGATT CCTGCTC

17

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGCACGATTC CTGCTCAA

18

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

TTCGCAAGAT TCCTATG

17

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CTTTCGCAAG ATTCCTAT

18

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

CTTTCGCAAG ATTCCTA

17

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

CTTTCGCAAG ATTCCTATG

19

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CTCTATGTAT CCCTCCT

17

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

TCTATGTATC CCTCCTG

17

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

CTCTATGTAT CCCTCCTGG

19

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CCTCTATGTA TCCCTCCT

18

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

CTGTACCAAA CCTTCGG

17

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CTGTACCAAA CCTTCG

16

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

GCTGTACCAA ACCTTCGG

18

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

TGTACCAAAC CTTGGAG

18

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

GGACCCTGCC GAACCT

16

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GGACCCTGCC GAACCG

16

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

GGGACCCTGC CGAAC

15

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

GGACCCTGCC GAAC

14

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GTTGCTGTTC AAAACCTT

18

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GTTGCTGTTC AAAACCTG

18

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

TGTTGCTGTT CAAAACCTG

19

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ATGTTGCTGT TCAAAACCTG

20

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

GATCCACGAC CACCA

15

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GGATCCACGA CCACCA

16

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GGATCCACGA CCACC

15

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GATCCACGAC CACCAGG

17

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TGTTCCAAAC CCTCGG

16

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

CTGTTCCAAA CCCTCG

16

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

CTGTTCCAAA CCCTCGG

17

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

GTTCCAAACC CTCGGAT

17

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GCCAAATCTG TGCAGC

16

(2) INFORMATION FOR SEQ ID NO: 187:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

CCAAATCTGT GCAGCAT

17

(2) INFORMATION FOR SEQ ID NO: 188:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GCCAAATCTG TGCAGCAG

18

(2) INFORMATION FOR SEQ ID NO: 189:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

GGCCAAATCT GTGCAGC

17

(2) INFORMATION FOR SEQ ID NO: 190:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ATCAACAACA ACCAGTA

17

(2) INFORMATION FOR SEQ ID NO: 191:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

GATCAACAAC AACCAGT

17

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

GATCAACAAC AACCAGTA

18

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

GGATCAACAA CAACCAGT

18

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

TCAAGGCAAC TCTATGTGG

19

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AGGTAAAGG TCCTTGT

17

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TAGGTAAAG GTCTTTGG

18

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TTAGGTAA GGTCTTT

17

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

GGTTAAAGGT CTTGTAGG

19

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

AGGTTAATGA TCTTTGT

17

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

TAGGTTAATG ATCTTTGG

18

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CTTTCGCAAG ATTCTATGG

20

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

GCTTTCGCAA GATTCCTATG

20

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

GCTTTCGCAA GATTCCTATG G

21

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CTTTCGCAAG ATTCCTATGG G

21

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GCTGTACCAA ACCTTCGGAG

20

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

TGCTGTACCA AACCTTCGG

19

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TGCTGTACCA AACCTTCGGA G

21

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

GCTGTACCAA ACCTTCGGAT

20

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TGGTTCGCCG GGCTTT

16

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

GTGGTTCGCC GGGCTTG

17

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GGTTCGCCGG GCTTTC

16

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

TGGTTCGCCG GGCTTTC

17

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

AGTGGTTCGC CGGGCTGG

18

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AGGATCCACG ACCACCAGG

19

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

AGGATCCACG ACCACCAGT

19

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CAGGATCCAC GACCACCAGG

20

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CTGTTCCAAA CCCTCGGAG

19

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CTGTTCCAAA CCCTCGGAT

19

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

GCTGTTCCAA ACCCTCGGAG

20

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

CTGAACCTTT ACCCCGTTGC

20

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

CTCGCCAACT TACAAGGCCT TTC

23

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AGAATGGCTT GCCTGAGTGC

20

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

GCTTTCGCAA GATTCCTATG GG

22

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 22 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GGCTTTCGCA AGATTCCTAT GG

22

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 23 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:



GGCTTTTCGCA AGATTCCTAT GGG

23

(2) INFORMATION FOR SEQ ID NO: 226:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

GGCTTTTCGCA AGATTCCTAT GGGG

24

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

CAGCTATATG GATGATGTG

19

(2) INFORMATION FOR SEQ ID NO: 228:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

AGCTATATGG ATGATGTGGG

20

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GCTATATGGA TGATGTGGT

19

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

AGCTATATGG ATGATGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CAGCTATATG GATGATATA

19

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGCTATATGG ATGATATAGG

20

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GCTATATGGA TGATATAGT

19

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AGCTATATGG ATGATATAGT

20

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CCATCATCTT GGGCTTG

17

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CATCATCTTG GGCTTT

16

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

CCATCATCTT GGGCTTT

17

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

CCATCATCTT GGGCTTTC

18

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

CCCCTGTCT GGCTTTC

17

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CCACTGTCTG GCTTTC

16

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCACTGTCTG GCTTT

15

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

CCCACTGTCT GGCTTG

16

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

TATATGGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TATGTGGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 245:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

TATATAGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 246:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TATATTGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 247:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

TATGTAGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

TATGTTCATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

TATATGGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

TATATGGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

TATGTGGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

TATGTGGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TATATAGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

TATATAGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

TATATTGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TATATTGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

TATGTAGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

TATGTAGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

TATGTTGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

TATGTTGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

TATATGGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

TATGTGGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

TATATAGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TATATTGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TATGTTAGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

TATGTTGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

TATGGGAGTG GGCCTCAG

18

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TATGGGATTG GGCCTCAG

18

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CAGTCCGTTT CTCTTGCC

18

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTCTGTTT CTCTTGGC

18

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

CAGTCCGTTT CTCATGGC

18

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTCTGTTT CTCATGGC

18

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CAGTCCGTTT CTCCTGGC

18

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGTCTGTTT CTCCTGGC

18

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

CAGCCCGTTT CTCCTGGC

18

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGCCTGTTT CTCCTGGC

18

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

CAGCCCGTTT CTCATGGC

18

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

CAGCCTGTTT CTCATGGC

18

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

AATTCCACTG CCTTCCACCA AGCTCTGCAG GATCCCAAAG TCAGGGGTCT GSTATCTTCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGCTCCGA ATATTGCCTC TCACATCTCG	120
TCAATCTCCG CGAGGACTGG GGACCCTGTG ACGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGGTC ACCCGTGTGT	300
CTTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GATTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GATCAACAAC AACCAGTACG GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGCAACT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTACGGATGG AAATTGCACC	600
TGTATTCCCA TCCCATCGTC CTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGCTAT ATGGATGATG TGGTATTGGG GGCCAAGACT GTACAGCATC	780
GTGAGTCCCT TTATACCGCT GTTACCAATT TTCTTTTGTC TCTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAAAGATGG GGTATTCCC TAAACTTCAT GGTCTACATA ATTGGAAGTT	900
GGGGAACATT GCCACAGGAT CATATTGTAC AAAAGATCAA ACACTGTTTT AGAAAACTTC	960
CTGTTAACAG GCCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCTCCATT TACTCAATGT GGATATCCTG CCTTAATGCC TTTGTATGCA TGTATACAAG	1080
CTAAACAGGC TTCACTTTC TCGCCAACTT ACAAGGCCTT TCTAAGTAAA CAGTACATGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCTG GTCTGTGCCA AGTGTTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AGCTCATCGG AACTGACAAT TCTGTCGTCC TCTCGCGGAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TACTGCCAAC TGGATCCTT GCGGGACGTC CTTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCTCGGG GCCGTTGGG AGTCTCTCGT CCCCTTCTCC	1500
GTCTGCCGTT CCAGCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTACCTCT GCACGTTGCA TGGAGACCAC	1620
CGTGAACGCC CATCAGATCC TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTTAAGG ACTGGGAGGA	1740
GCTGGGGGAG GAGATTAGGT TAAAGGTCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTTAC CTCTGCCTAA TCATCTCTTG TACATGTCCC	1860

ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTACTGT GGAGTTACTC TCGTTTTTGC CTTCTGACTT CTTTCCTTCC	1980
GTCAGAGATC TCCTAGACAC CGCCTCAGCT CTGTATCGAG AAGCCTTAGA GTCTCCTGAG	2040
CATTGCTCAC CTCACCATAC TGCCTCAGG CAAGCCATTC TCTGCTGGGT GGAATTGATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTTG GAAGATCCAG CATCCAGGGA TCTAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGTTTAAAG ATCAGGCAAC TATTGTGGTT TCATATATCT	2220
TGCCTTACTT TTGGAAGAGA GACTGTGCTT GAATATTTGG TCTCTTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGGGA CCGAGGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400
AGACGCAGAT CTCAATCGCC GCGTCGCAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCCTTGG ACTCATAAGG TGGGAACTT TACTGGGCTT TATTCCTCTA CAGTACCTAT	2520
CTTTAATCCT GAATGGCAA CTCCTTCCTT TCCTAAGATT CATTTACAAG AGGACATTAT	2580
TAATAGGTGT CAACAATTTG TGGGCCCTCT CACTGTAAAT GAAAAGAGAA GATTGAAATT	2640
AATTATGCCT GCCAGATTCT ATCCTACCCA CACTAAATAT TTGCCCTTAG ACAAAGGAAT	2700
TAAACCTTAT TATCCAGATC AGGTAGTTAA TCATTACTTC CAAACCAGAC ATTATTTACA	2760
TACTCTTTGG AAGGCTGGTA TTCTATATAA GAGGGAAACC ACACGTAGCG CATCATTTTG	2820
CGGGTCACCA TATTCTTGGG AACAGAGCT ACAGCATGGG AGGTGGTCA TCAAAACCTC	2880
GCAAAGGCAT GGGGACGAAT CTTTCTGTTC CCAACCCTCT GGGATTCTTT CCCGATCATC	2940
AGTTGGACCC TGCATTGGA GCCAACTCAA ACAATCCAGA TTGGGACTTC AACCCCATCA	3000
AGGACCACTG GCCAGCAGCC AACCAGGTAG GAGTGGGAGC ATTCGGGCCA AGGCTCACCC	3060
CTCCACACGG CGGTATTTTG GGGTGGAGCC CTCAGGCTCA GGGCATATTG ACCACAGTGT	3120
CAACAATTCC TCCTCCTGCC TCCACCAATC GGCAGTCAGG AAGGCAGCCT ACTCCCATCT	3180
CTCCACCTCT AAGAGACAGT CATCCTCAGG CCATGCAGTG G	3221

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AATCCACTG CCTGCACCA AGCTCTGCAG GATCCCAGAG TCAGGGGTCT GTATCTTCCT

GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGCTCCGA ATATTGCCTC TCACATCTCG	120
TCAATCTCCG CGAGGACTGG GGACCCTGTG ACGATCATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGATC ACCCGTGTGT	300
CTTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTATT GGTTCCTTG GATTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GATCAACAAC AACCAGTACG GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGCAACT CTAAGTTTCC CTCATGTTGC TGTACAAAAC CTACGGATGG AAATTGCACC	600
TGTATTCCCA TCCCATCGTC CTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTCGTTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGCTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGCATC	780
GTGAGTCCCT TTATACCGCT GTTACCAATT TTCTTTTGT TCTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAAAGATGG GGTATTCCC TAAACTTCAT GGGCTACATA ATTGGAAGTT	900
GGGGAACCTT GCCACAGGAT CATATTGTAC AAAAGATCAA ACACTGTTTT AGAAACTTC	960
CTGTTAACAG GCCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCTCCATT TACACAATGT GGATATCCTG CCTTAATGCC TTTGTATGCA TGTATACAAG	1080
CTAAACAGGC TTTCACCTTC TCGCCAACTT ACAAGGCCTT TCTAAGTAAA CAGTACATGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCTG GTCTGTGCCA AGTGTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTAGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AGCTCATCGG AACTGACAAT TCTGTCTGTC TCTCGCGGAA ATATACATCA TTTCCATGGC	1380
TGCTAGGCTG TACTGCCAAC TGGATCCTTC GCGGGACGTC CTTTGTGTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCTCGGG GCCGCTTGGG ACTCTCTCGT CCCCTTCTCC	1500
GTCTGCCGTT CCAGCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTCACTCT GCACGTTGCA TGGCGACCAC	1620
CGTGAACGCC CATCAGATCC TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCCCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTTAAGG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGGT TAATGATCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTTAC CTCTGCCTAA TCATCTCTTG TACATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCCTAT	1920
AAAGAATTTG GAGCTACTGT GGAGTTACTC TCGTTTTTGC CTTCTGACTT CTTTCTCTCC	1980
GTACGAGATC TCCTAGACAC CGCCTCAGCT CTGTATCGAG AAGCCTTAGA GTCTCCTGAG	2040

CATTGCTCAC CTCACCATAC TGCACCTCAGG CAAGCCATTC TCTGCTGGGG GGAATTGATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTTG CAAGATCCAG CATCCAGAGA TCTAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGTTTAAAG ATCAGGCAAC TATTGTGGTT TCATATATCT	2220
TGCCTTACTT TTGGAAGAGA GACTGTACTT GAATATTTGG TCTCTTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGGGA CCGAGGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400
AGACGCAGAT CTCAATCGCC GCGTCGCAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCCTTGG ACTCATAAGG TCGGAACTT TACGGGGCTT TATTCCTCTA CAGTACCTAT	2520
CTTTAATCCT GAATGGCAAA CTCCTTCCTT TCCTAAGATT CATTTACAAG AGGACATTAT	2580
TAATAGGTGT CAACAATTTG TGGGCCCTCT CACTGTAAAT GAAAAGAGAA GATTGAAATT	2640
AATTATGCCT GCTAGATTCT ATCCTACCCA CACTAAATAT TTGCCCTTAG ACAAAGGAAT	2700
TAAACCTTAT TATCCAGATC AGGTAGTTAA TCATTACTTC CAAACCAGAC ATTATTTACA	2760
TACTCTTTGG AAGGCTGGTA TTCTATATAA GAGGGAAACC ACACGTAGCG CATCATTTTG	2820
CGGGTCACCA TATTCTTGGG AACAAGAGCT ACAGCATTCG CAAAGGCATG GGGACGAATC	2880
TTTCTGTTCC CAACCCTCTG GGATTCTTC CCGATCATCA GTTGGACCCT GCATTTCGGAG	2940
CCAACTCAAC AAATCCAGAT TGGGACTTCA ACCCCATCAA GGACCACTGG CCAGCAGCCA	3000
ACCAGGTAGG AGTGGGAGCA TTCGGGCCAG GGCTCACCCC TCCACACGGC GGTATTTTGG	3060
GGTGGAGCCC TCAGGCTCAG GGCATATTGA CCACAGTGTC AACAATTCCT CTCCTGCCT	3120
CCACCAATCG GCAGTCAGGA AGGCAGCCTA CTCCCATCTC TCCACCTCTA AGAGACAGTC	3180
ATCCTCAGGC CATGCAGTGG	3200

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3221 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AATTCCACTG CTTCCACCA AGCTCTGCAA GACCCAGAG TCAGGGGTCT GTATTTTCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGCTCCGA ATATTGCCTC TCACATCTCG	120
TCAATCTCCG CGAGGACCGG GGACCCTGTG ACGAACATGG AGAACATCAC ATCAGGATTC	180

CTAGGACCCC TGCCCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGATC ACCCGTGTGT	300
CTTGGCCAAA ATTCGCGATC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTATT GGTTCTTCTG GATTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCTAG GATCAACAAC AACCAGTACG GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGCAACT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTACGGATGG AAATTGCACC	600
TGTATTCCCA TCCCATCGTC TTGGGCTTTC GCAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTTCACT GGTTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGCTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGCATC	780
GTGAGTTCCT TTATACCGCT GTTACCAATT TTCTTTTGTG TCTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAAAGATGG GGTATTCCC TAAACTTCAT GGGTTATGTA ATTGGAAGTT	900
GGGGAACATT GCCACAGGAT CATATTGTAC AAAAAATCAA ACACTGTTTT AGAAAACCTC	960
CTGTTAACAG GCCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCTCCTTT TACACAATGT GGATATCCTG CCTTAATGCC CTTGTATGCA TGTATACAAG	1080
CTAAACAGGC TTTCACCTTC TCGCCAACCT ACAAGGCCCT TCTAAGTAAA CAGTACATGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCTG GTCTGTGCCA AGTATTTGCT GATGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATAGGCCATC AGCGCATGCG CGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCCGG TCTGGAGCGA	1320
AACTCATCGG AACTGACAA TCTGTCTGCC TCTCGCGGAA ATATACCTCG TTTCCATGGC	1380
TACTAGGCTG TGCTGCCAAC TGGATCCTTC GCGGGACGTC CTTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCTCGGG GCCGCTTGGG ACTCTCTCGT CCCCTTCTCC	1500
GTCTGCCGTT CCAGCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTACCTCT GCACGTTGCA TGGAGACCAC	1620
CGTGAACGCC CATCAGATCC TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCCCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTTAAGG ACTGGGAGGA	1740
GCTGGGGGAG GAGATTAGGT TAAAGGTCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTTAC CTCTGCCTAA TCATCTCTTG TACATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTACTGT GGAGTTACTC TCGTTTTTGC CTTCTGACTT CTTTCCTTCC	1980
GTCAGAGATC TCCTAGACAC CGCCTCGGCT CTGTATCGGG AAGCCTTAGA GTCTCCTGAG	2040
CATTGCTCAC CTCACCATAC CGCACTCAGG CAAGCCATTC TCTGCTGGGG GGAATTGATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTTG GAAGATCCAG CATCCAGGGA TCTAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGATTAAAG ATCAGGCAAC TCTTGTGGTT TCATATCTCT	2220

TGCCTTACTT TTGGAAGAGA AACTGTACTT GAATATTTGG TCTCTTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAAACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGGGA CCGAGGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400
AGACGCAGAT CTCAATCGCC GCGTCGCAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCCTTGG ACTCATAAGG TGGGAAACTT CACTGGGCTT TATTCCTCTA CAGCACCTAT	2520
CTTTAATCCT GAATGGCAA CTTCTTCCTT TCCTAAATTT CATTTACAAG AGGACATTAT	2580
TAATAGGTGT CAACAATTTG TGGGCCCTCT CACTGTAAAT GAAAAGAGAA GATTGAAATT	2640
AATTATGCCT GCTAGATTCT ATCCTACCCA CACTAAATAT TTGCCCTTAG ACAAAGGAAT	2700
TAAACCTTAT TATCCAGATC AGGTAGTTAA TCATTACTTC CAAACCAGAC ATTATTTACA	2760
TACTCTTTGG AAGGCGGGTA TTCTATATAA GAGAGAAACC ACACGTAGCG CATCATTTTG	2820
CGGGTCACCA TATTCTTGGG AACAAGAGCT ACAGCATGGG AGGTTGGTCA TCAAAACCTC	2880
GCAAAGGCAT GGGGACGAAT CTTTCTGTTC CCAACCCTCT GGGATTCTTT CCCGATCATC	2940
AGTTGGACCC TGTATTCGGA GCCAACTCAA ACAATCCAGA TTGGGACTTC AACCCCATCA	3000
AGGACCACTG GCCAGCAGCC AACCAGGTAG GAGTGGGAGC ATTCGGGCCA GGGTTCACCC	3060
CTCCACACGG CGGTGTTTTG GGGTGGAGCC CTCAGGCTCA GGGCATGTTG ACCCCAGTGT	3120
CAACAATTCC TCCTCCTGCC TCCGCCAATC GGCAGTCAGG AAGGCAGCCT ACTCCCATCT	3180
CTCCACCTCT AAGAGACAGT CATCCTCAGG CCATGCAGTG G	3221

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AATTCCACTG CTTTCCACCA AGCTCTGCAG GATCCCAGAG TCAGGGGTCT GTATCTTCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGCTCCGA ATATTGCCTC TCACATCTCG	120
TCAATCTCCG CGAGGACTGG GGACCCTGTG ACGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGGTC ACCCGTGTGC	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAATT	360

TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTATT GGTCTTCTG GATTATCAAG GTATGTTGCC CGTTTGTCTT	480
ATAATTCCAG GATCAACAAC AACCAGTACG GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGCAACT CTTTGTTTCC CTCATGTTGE TGTACAAAAC CTACGGATGG AAATTGCACC	600
TGTATTCCCA TCCCATCGTC CTGGGCTTTC GCAAAATACC TATGGGAGCG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTTCAGT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTTAGCTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGCATC	780
GTGAGGCCCT TTATACCGCT GTTACCAATT TTCTTTTGTC TCTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAAAGATGG GGTATTCCC TAAACTTCAT GGGTTACAGA ATTGGAAGTT	900
GGGGAACATT GCCACAGGAT CACATTGTAC AAAAGATCAA ACACTGTTTT AGAAAACCTC	960
CTGTTAACAG GCCTATTGAT TGGAAGGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCTCCTTT TACACAATGT GGATATCCTG CCTTAATGCC TTTGTATGCA TGTATACAAG	1080
CTAAACAGGC TTTCTCTTTC TCGCCAACCT ACAAGGCCTT TCTAAGTAA CAGTACCTGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCTG GTCTGTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTAGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AGCTCATCGG AACTGACAAT TCTGTCGTCC TCTCGCGGAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTTC GCGGGACGTC CTTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCTCGGG GCCGCTTGGG ACTCTATCGT CCCCTTCTCC	1500
GTCTGCCGTT CCAGCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTACCTCT GCACGTTGCA TGGAGACCAC	1620
CGTGAACGCC CATCAGAGCC TGCCCAAGGT CTTACATAAG AGAACTCTTG GACTCCCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTTAAGG ACTGGGAGGA	1740
GCTGGGGGAG GAGATTAGGT TAATGATCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCTTG TTCATGTCTC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGAG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTAGTGT GGAGTTACTC TCGTTTTTGC CTCATGACTT CTTTCCTTCC	1980
GTCAGAGATC TCCTAGACAC CGCCTCAGCT CTGTATCGAG AAGCCTTAGA GTCTCCTGAG	2040
CATTGCTCAC CTCACCATAC TGCACTCAGG CAAGCCGTTT TCTGCTGGGG GGAATTAATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTG CAAGATCCAG CATCCAGGGA TCAAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGTTTAAAG ATCAGGCAAC TATTGTGGTT TCATATATCT	2220
TGTCTTATGT TTGGAAGAGA CACTGTACTT GAATATTTGG TCTCTTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GATGTCGGGA CCGACGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400



AGACGCAGAT CTCAATCGCC GCGTCGAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCCTTGG ACTCATAAGG TGGGAAACTT TACTGGGCTT TATTCCTCTA CAGTACCTAT	2520
CTTTAATCCT GAATGGCAAA CTCCTTCCTT TCCTAAGATT CATTTACAAG AGGACATTAT	2580
TAATAGGTGT CAACAATTTG TGGGCCCTCT TACTGTAAAT GAAAAGAGAA GATTGAAATT	2640
AATTATGCCT GCTAGATTCT ATCCTACCCA CACAAAATAT TTGCCCTTAG ACAAAGGAAT	2700
TAAACCTTAT TATCCAGATC AGGTAGTTAA TCATTACTTC CAAACCAGAC ACTATTTACA	2760
TACTCTTTGG AAGGCTGGTA TTCTATATAA GAGGGAACCC ACACGTAGCG CATCATTTTC	2820
CCGGTCACCA TATTCTTGGG AACAAAGAGCT ACAGCATGGG AGGTGGGACA TCAAAACCTC	2880
GCAAAGGCAT GGGGACGAAT CTTTCTGTTC CCAACCCTCT GGGATTCTTT CCCGATCATC	2940
AGTTGGACCC TGCATTCEGA GCCAACTCAA ACAATCCAGA TTGGGACTTC AACCCCATCA	3000
AGGACCACTG GCCAGCAGCC AACCAGGTGG GAGTGGGAGC ATTCGGGCCA GGGCTCACCC	3060
CTCCACACGG CGGTATTTTG GGGTGGAGCC CTCAGGCTCA AGGCATATTG ACCACAGTGT	3120
CAACAATTCC TCCTCCTGCC TCCACCAATC GGCAGTCAGG AAGGCAGCCT ACTCCCATCT	3180
CTCCACCTCT GAGAGAAAGT CATCCTCAGG CCATGCAGTG G	3221

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3221 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AATTCACAG CTTTCCACCA AGCTCTGCAA GATCCCAGAG TCAGGGGCCT GTATTTTCCT	60
GCTGGTGGCT CCAGTTCAGG AACACTCAAC CCTGTTCCAA CTATTGCCTC TCACATCTCG	120
TCAATCTCCT CGAGGATTGG GGACCCTGCA CCGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCGTGTGT	300
CTTGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTATT GGTTCTTCTG GATTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCAG GATCAACAAC AACCAGCAGG GGACCCTGCA AAACCTGCAC GACTCCTGCT	540

CAAGGCAACT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTACGGATGG AAATTGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGCTAT ATGGATGATG TGGTACTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATACCGCT GTTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAGAGATGG GGTTATTCCC TGAATTTTCAT GGGTTATGTA ATTGGAAGTT	900
GGGGTACATT GCCACAGGAT CATATTGTAC AAAAAATCAA ACACTGTTTT AGAAAACTTC	960
CTGTTAATCG ACCTATTGAT TGGAAAGTAT GTCAGAGACT TGTAGGTCTT TTAGGCTTTG	1020
CCGCTCCATT TACACAATGT GGTTACCCTG CATTAATGCC TTTGTATGCA TGTATACAAG	1080
CGAAACAGGC TTTTACTTTC TCGCCAACTT ACAAGGCCTT TCTAAGTAAA CAGTATATGA	1140
ACCTTTACCC CGTTGCCCCG CAACGGCCTG GTCTGTGCCA AGTGTTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATCGGCCATC AGCGCATGCG TGAAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCAGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AACTCATCEG GACTGACAAT TCTGTCGTCC TTTCTCAGAA ATATACATCC TTTCCATAGC	1380
TGCTAGGTTG TACTGCCAAC TAGATTCTTC GCGGGACGTC CTTTGTCTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCGCGAG GCCGCTTGGG ACTGTATCGT CCCCTTCTCC	1500
GTCTGCCGTA CCGTCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTACCTCT GCACGTTGCA TGGAGACCAC	1620
CGTGAACGCC CATCAGGTCC TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGGT TAAAGGTCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA TTATCATGCA ACTTTTTTAC CTCTGCCTAA TCATCTCTTG TACATGTCCC	1860
ACTTTTCAAG CCTCCAAGCT GTGCCTTGGA TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG AGCTACTGTG GAGTTACTCT CATTTTTGCC TTCTGACTTC TTTCTTCCG	1980
TCCGGGATCT ACTAGAATAC AGCCTCAGCT CTATATCGGG AAGCCTTAGA GTCTCCTGAG	2040
CATTGCTCAC CTCACCATAC AGCACTCAGG CAAGCCATTC TCTGCTGGGG GAAATTAATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTTG GAAGATCCAG CATCCAGGGA TCTAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGCCTAAAG ATCAGGCAAT TATTGTGGTT TCATATTTCT	2220
TGCCTTACTT TTGGAAGAGA AACTGTCCTT GAGTATTTGG TCTCTTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGA CCGAGGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400
AGACGCAGAT CTCAATCGCC GCGTCGCAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCCTTGG ACTCATAAGG TGGGAAATTT TACTGGGCTT TATTCTTCTA CTGTCCCTAT	2520
CTTTAATCCT GAATGGCAAA CACCTTCTTT TCCTAAATTT CATTTACATG AAGACATTGC	2580

TAATAGGTGT CAGCAATTTG TAGGCCCTCT CACTGTAAAT GAAAAAGAA GACTGAAATT	2640
AATTATGCCT GCTAGGTTTT ATCCTAACAG CACAAAATAT TTGCCCTTAG ACAAAGGGAT	2700
TAAAACTTAT TATCCTGATC ATGTAGTTAA TCATTACTTT CAAACCCGAC ATTATTTACA	2760
TACTCTTTGG AAGGCTGGGA TTCTATATAA GAGGGAAACT ACACGTAGCG CCTCATTTTG	2820
CGGGTCACCA TATTCTTGGG AACAAGAGCT ACATCATGGG AGGTTGGTCA TCAAAACCTC	2880
GCAAAGGCAT GGGGACGAAC CTTTCTGTTC CCAACCCTCT GGGATTCTTT CCCGATCATC	2940
AGTTGGACCC TGCATTCGGA GCCAATTCAA ACAATCCAGA TTGGGACTTC AACCCCATCA	3000
AGGACCACTG GCCACAAGCC AACCAGGTAG GAGTGGGAGC ATTTGGGCCA GGGTTCACTC	3060
CCCCACACGG AGGTGTTTTG GGGTGGAGCC CTCAGGCTCA GGGCATATTG GCCACCGTGC	3120
CAGCGATGCC TCCTCCTGCC TCCACCAATC GGCAGTCAGG AAGGCAGCCT ACTCCCATCT	3180
CTCCACCTCT AAGAGACAGT CATCCTCAGG CCATGCAGTG G	3221

(2) INFORMATION FOR SEQ ID NO: 284:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

AACTCCACCA CGTTCCACCA AACTCTTCAA GATCCCAGAG TCAGGGCTCT GTACTTTCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTTACA AACTGCCTC TTCCATATCG	120
TCAATCTTAT CGACGACTGG GGACCCGTG CCGAACATGG AGAACATCGC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTCGT TGACAAAAAT CCTCACAATA	240
CCTCTGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGAAAC ACCCGTGTGT	300
CTTGGCCAAA ATTTCGAGTC CCAAATCTCC AGTCACTCAC CAACTTGTTG TCCTCCGATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTG CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GATCATCAAC CACCAGCACA GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTACGGACGG AAACTGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTTCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTCAGTTAT ATGGATGATG TGGTTTTGGG GGCCAAGTCT GTACAACATC	780

TTGAGTCCCT	TTATGCCGCT	GTTACCAATT	TTCTTTTGTC	TTTGGGTATA	CATTTAAACC	840
CTCAGAAAAC	AAAAAGATGG	GGCTACTCCC	TTAACTTCAT	GGGGTATGTA	ATTGGAAGTT	900
GGGGGACCTT	ACCCCAAGAA	CATATTGTGT	TGAAAATCAA	ACAATGTTTT	AGGAAACTTC	960
CTGTAAACAG	GCCTATTGAT	TGGAAAGTAT	GTCAACGAAT	TGTGGGTCTT	TTGGGATTTG	1020
CTGCTCCTTT	CACACAATGT	GGATATCCTG	CTTTAATGCC	TTTATATGCA	TGTATACAAG	1080
CTAAACAGGC	TTTTACTTTT	TCGCCAACGT	ATAAGGCCTT	TCTAAACAAA	CAATATCTGA	1140
ACCTTTACCC	CGTTGCTCGG	CAACGGCCAG	GTCTGTGCCA	AGTGTTTGCT	GACGCAACCC	1200
CCACTGGCTG	GGGCTTGGCC	ATAGGCCATC	AGCGCATGCG	TGGGACCTTT	GTGTCTCCTC	1260
TGCCGATCCA	TACTGTGGAA	CTCCTAGCAG	CTTGTTTTGC	TCGCAGCAGG	TCTGGAGCAA	1320
AACTTATCGG	GACTGACAAT	TCTGTCTGCC	TTTCCCGCAA	ATATACATCG	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTTGTCTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCCTCCCGGG	GCCGCTTGGG	GCTCTACCGC	CCGCTTCTCC	1500
GCCTGCCGTA	CCGTCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGACTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CATCGGAACC	TGCCCCAAGG	CTTGCATAAG	AGGACTCTTG	GACTTTCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCACACTT	CAAAGACTGT	GTGTTTACTG	AGTGGGAGGA	1740
GTTGGGGGAG	GAGATCAGGT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGTTCACCA	GCACCATGCA	ACTTTTTCAC	CTCTGCCTAA	TCATCTCATG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTGGG	GCATGGACAT	TGACCCGTAT	1920
AAAGAATTTG	GAGCTTCTGT	GGAGTTACTC	TCTTTTTTGC	CTTCTGACTT	CTTTCCTTCT	1980
ATTCGAGATC	TTCTCGACAC	CGCCTCTGCT	CTGTATCGGG	AGGCCTTAGA	GTCTCCGGAA	2040
CATTGTTCAC	CTCACCATAC	GGCACTCAGG	CAAGCTATTC	TGTGTTGGGG	TGAGTTGATG	2100
AATCTAGCCA	CCTGGGTGGG	AAGTAATTTG	GAAGACCCAG	CCTCCCGGGA	ATTAGTAGTC	2160
AGTTATGTCA	ATGTTAATAT	GGGCCTAAAA	ATCAGACAAC	TATTGTGGTT	TCACATTTCC	2220
TGTCTTACGT	TTGGAAGAGA	AACTGTTCTT	GAATATTTGG	TGTCTTTTGG	AGTGTGGATT	2280
CGCACACCTC	CAGCATATAG	ACCACCAAAT	GCCCCATCT	TATCAAACT	TCCGGAAACT	2340
ACTGTTGTTA	GACGACGAGG	CAGGTCCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGGTCTCAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCGGG	AATCTCAATG	TTAGTATTCC	2460
TTGGACTCAT	AAGGTGGGAA	ACTTTACGGG	GCTTTATTCT	TCTACGGTAC	CTAGCTTTAA	2520
TCCTCAATGG	CAAACCTCCT	CATTTCCCTGA	CATTCATTG	CAGGAGGACA	TCATTAATAA	2580
GTGTAAACAA	TTTGTGGGAC	CCCTTACAGT	GAATGAAAAA	AGGAGACTAA	AATTGATTAT	2640
GCCTGCTAGG	TTCTATCCCA	ATGTTACTAA	ATATTTGCCC	TTAGATAAAG	GAATTAAACC	2700
TTATTATCCA	GAGCATGTAG	TTAATCATTA	CTTCCAGACG	AGACATTATT	TACATACTCT	2760

TTGGAAGGCG GGTATCTTAT ATAAAAGAGA GACAACACGT AGCGCCTCAT TTTGCGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCCTCCAAA CCTCGACAAG	2880
GCATGGGGAC AAATCTTTCC GTCCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940
ACCCTGCATT CAAAGCCAAC TCCGACAATC CCGATTGGGA CCTCAACCCA CACAAGGACA	3000
ACTGGCCGGA CTCCAACAAG GTGGGAGTGG GAGCATTCTGG GCCGGGATTC ACTCCACCCC	3060
ATGGGGGACT GTTGGGGTGG AGCCCTCAAG CTCAGGGCAT ACTCACAACCT GTGCCAACAG	3120
CTCCTCCTCC TGCCTCCACC AATCGGCAGT TAGGAAGGAA GCCTACTCCC CTGTCTCCAC	3180
CTCTAAGAGA CACTCATCCT CAGGCAATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

AACTCCACCA CGTTCACCA AACTCTTCAA GATCCCAGAG TCAGGGCTCT GTACTTTCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTTCTG AACTGTCTC TTCCATATCG	120
TCAATCTTAT CGAAGACTGG GGACCCTGTG CCGAATATGG AGAATATCGC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGTG ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC ACCCGTGTGT	300
CTTGGCCAAA ATTTCGAGTC CCAAATCTCC AGTCACTCAC CAACTTGTG TCCTCCGATT	360
TGTCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCTCTG CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTG GGTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCAG GATCATCAAC CACCAGCACC GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTACGGACGG AACTGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTC GCAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTTCTG GTTTCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTTCTTAT ATGGATGATG TGGTTTTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATGCCGCT GTTACCAATT TTCTTTTGTG TTTGGGTATA CATTAAACC	840
CTCAGAAAAC AAAAAGATGG GGCTACTCCC TCAACTTCAT GGGGTATGTA ATTGGAAGTT	900
GGGGCACCTT ACCCCAAGAA CATATTGTGT TGAAACTCAA ACAATGCTTT AGAAACTTC	960

CTGTAAACAG ACCTATTGAT TGGAAGGTGT GTCAACGAAT TGTGGGTCTT TTGGGATTTG	1020
CTGCTCCTTT CACACAATGT GGTATCCTG CTTTAATGCC TTTATATGCA TGTATACAAG	1080
CTAAACAGGC TTTTACTTTT TCGCCAACGT ATAAGGCCTT TCTAACCAAA CAATATCTGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCAG GTCTGTGCCA AGTGTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGTCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCAGG TCTGGAGCAA	1320
AACTTATCGG GACTGACAAT TCTGTTGTCC TTTCCCGCAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTGTCTAC GTTCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCCCGGG GCCGCTTGGG GCTCTACCGC CCGCTTCTCC	1500
GTCTGCCGTA CCGACCGACC ACGGGGCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCGTCT GCCGGACCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CATCGGAACC TGCCCAAGGT CTTGCATAAG AGGACTCTTG GACTTTCAGC	1680
AATGTCACCG ACCGACCTTG AGGCATACTT CAAAGACTGT GTGTTTACTG AGTGGGAGGA	1740
GTTGGGGGAG GAGATCAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTTG GAGCTTCTGT GGAGTTACTC TCTTTTTTGC CTTCTGACTT CTTTCTTCT	1980
ATTCCGATC TTCTCGACAC CGCCTCTGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTAC CTCACCATAC GGCATCAGG CAAGCTATTT TGTGTTGGGG TGAGTTGATG	2100
AATCTAGCCA CCTGGGTGGG AAGTAATTTG GAAGACCCAG CATCCCGGGA ATTAGTAGTC	2160
AGTTATGTCA ATGTTAATAT GGGCCTAAAA ATCAGACAAC TATTGTGGTT TCACATTTCC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAATATTTGG TGTCTTTTGG AGTGTGGATT	2280
CGCACACCTC CTGCATATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCTCACC TCGCAGACGA	2400
AGGTCTCAAT CGCCCGGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGAATCAT AAGGTGGGAA ACTTTACGGG GCTTTATTCT TCTACGGTAC CTAGCTTTAA	2520
TCCTAAATGG CAACTCCTT CCTTTCCTGA CATTCAATTG CAGGAGGATA TCATTAATAG	2580
GTGTGAACAA TTTGTGGGAC CCCTCACAGT GAATGAAAAC AGGAGACTAA AATTGATTAT	2640
GCCTGCTAGG TTCTATCCCA ATGTTACTAA ATATTTGCCC TTAGATAAAG GAATCAAACC	2700
TTATTATCCA GAGCATGTAG TTAATCATTA CTTCCAGACG AGACATTATT TACATACTCT	2760
TTGGAAGGCG GGTATCTTAT ATAAAAGAGA GACAACACGT AGCGCCTCAT TTTGCGGGTC	2820
ACCATATTCT TGGGAACAAG ATCTACAGCA TGGGAGGTTG GTCCCTCAAA CCTCGACAAG	2880
GCATGGGGAC AAATCTTTCC GTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940

ACCCTGCATT CAAAGCCAAC TCCGACAATC CCGATTGGGA CCTCAACCCA CACAAGGACA	3000
ACTGGCCGGA CTCCAACAAG GTGGGAGTGG GAGCATTCGG GCCGGGATTC ACTCCACCCC	3060
ATGGGGGACT GTTGGGGTGG AGCCCTCAAG CTCAGGGCAT ACTCACAACCT GTGCCAACAG	3120
CTCCTCCTCC TGCCTCCACC AATCGGCAGT TAGGAAGGAA GCCTACTCCC CTGTCTCCAC	3180
CTCTAAGAGA CACTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

AACTCCACCA CTTTCCACCA AACTCTTCAA GATCCCAGAG TCAGGGCTCT GTACTTTCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAGC CCTGCTCAGA ATACTGTCTC AGCCATATCG	120
TCAATCTTAT CGAAGACTGG GGACCCTGTG CCGAACATGG AGAACATCGC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC ACCCGTGTGT	300
CTTGCCAAA ATTTCGAGTC CCAAATCTCC AGTCACTCAC CAACCTGTTG TCCTCCAATT	360
TGTCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TCTTCCTCTG CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCAG GATCATCAAC CACCAGCAGG GGACCATGCA AGACCTGCAC AACTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTATGGATGG AACTGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTTCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTTCAATTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATGCCGCT GTTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAAAGATGG GGATATTCCC TTAACCTCAT GGGATATGTA ATTGGGAGTT	900
GGGGCACATG GCCACAGGAT CATATTGTAC AAAACTTCAA ACTATGTTTT AGAAAACCTC	960
CTGTAAACAG GCCTATTGAT TGGAAAGTTT GTCAACGAAT TGTGGGTCTT TTGGGGTTTG	1020
CTGCCCCCTT TACGCAATGT GGATATCCTG CTTTAATGCC TTTATATGCA TGTATACAAG	1080
CAAAACAGGC TTTTACTTTC TCGCCAACTT ACAAGGCCTT TCTCAGTAAA CAGTATATGA	1140

CCCTTTACCC	CGTTGCTCGG	CAACGGCCTG	GTCTGTGCCA	AGTGTGCT	GACGCAACCC	1200
CCACTGGTTG	GGGCTTGGCC	ATAGGCCATC	AGCGCATGCG	TGGAACCTTT	GTGTCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTTTTGC	TCGCAGCAGG	TCTGGAGCAA	1320
ACCTCATCGG	GACCGACAAT	TCTGTCTGAC	TCTCCCGCAA	GTATACATCG	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTTGTTTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCCTCCCGGG	GCCGCTTGGG	GCTCTACCGC	CCGCTTCTCC	1500
GTCTGCCGTA	CCGTCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGACTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CACCGGAACC	TGCCCAAGGT	CTTGCATAAG	AGGACTCTTG	GACTTTTCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	GTGTTTAATG	AGTGGGAGGA	1740
GCTGGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTACTCGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGTTACCA	GCACCATGCA	ACTTTTTTAC	CTCTGCCTAG	TCATCTCTTG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTGGG	GCATGGACAT	TGACCCCTAT	1920
AAAGAATTTG	GAGCTACTGT	GGAGTTACTC	TCTTTTTTGC	CTTCTGACTT	CTTTCCGTCG	1980
GTGCGGGACC	TCCTAGATAC	CGTCTCTGCT	CTGTATCGGG	AAGCCTTAAA	ATCTCCTGAG	2040
CATTGCTCAC	CTCACCACAC	AGCACTCAGG	CAAGCTATTC	TGTGCTGGGG	GGAATTAATG	2100
ACTCTAGCTA	CCTGGGTGGG	TAATAATTTG	GAAGATCCAG	CATCCCGGGA	TCTAGTAGTC	2160
AATTATGTTA	ACACTAACAT	GGGCCTAAG	ATCAGGCAAC	TATGGTGGTT	TCACATTTCC	2220
TGTCTTACTT	TTGGAAGAGA	AACTGTTCTG	GAATATTTGG	TATCTTTTGG	AGTGTGGATT	2280
CGCACTCCTC	CTGCCTACAG	ACCACCAAAT	GCCCCATCT	TATCAACACT	TCCGGAAACT	2340
ACTGTTGTTA	GACGACGAGG	CAGGTCCCTT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGGTCTCAAT	CACCGCGTCG	CAGAAGATCT	CAATCTCGGG	AATCCCAATG	TTAGTATCCC	2460
TTGGACTCAT	AAGGTGGGAA	ACTTTACGGG	GCTTTATTCT	TCTACAGTAC	CTGTCTTTAA	2520
TCCTGAATGG	CAAACCTCCT	CTTTTCCAGA	CATTCAATTA	CAGGAGGACA	TTGTTGATAG	2580
ATGTAAGCAA	TTTGTGGGAC	CCCTTACAGT	AAATGAAAAC	AGGAGACTAA	AATTAATAAT	2640
GCCTGCTAGA	TTTTATCCCA	ATGTTACCAA	ATATTTGCCC	TTAGATAAAG	GTATCAAACC	2700
TTATTATCCA	GAGCATGTAG	TTAATCATT	CTTCCAGACT	AGACATTATT	TGCATACTCT	2760
TTGGAAGGCG	GGTATCTTAT	ATAAAAGAGA	GTCAACACAT	AGCGCCTCAT	TTTGCGGGTC	2820
ACCTTATTCT	TGGGAACAAG	ATCTACAGCA	TGGGAGGTTG	GTCTTCCAAA	CCTCGAAAAG	2880
GCATGGGGAC	AAATCTTTCT	GTCCCCAATC	CCCTGGGATT	CTTCCCCGAT	CATCAGTTGG	2940
ACCCTGCATT	CAAAGCCAAC	TCAGAAAATC	CAGATTGGGA	CCTCAACCCA	CACAAGGACA	3000
ACTGGCCGGA	CGCCCACAAG	GTGGGAGTGG	GAGCATTCGG	GCCAGGATTC	ACCCCTCCCC	3060
ATGGGGGACT	GTTGGGGTGG	AGCCCTCAGG	CTCAGGGCAT	ACTCACATCT	GTGCCAGCAG	3120



CTCCTCCTCC TGCCTCCACC AATCGGCAGT CAGGACGGCA GCCTACTCCC CTATCTCCAC 3180  
CTCTAAGGGA CACTCATCCT CAGGCCATGC AGTGG 3215

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

AACTCCACCA CTTTCCACCA AACTCTTCAA GATCCCGGAG TCAGGGCCCT GTACTTTCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTGAGC CCGCTCAGA ATACTGTCTC TGCCATATCG	120
TCAATCTTAT CGAAGACTGG GGACCCTGTA CCGAACATGG AGAACATCGC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC ACCCGTGTGT	300
CTTGCCAAA ATTGCGAGTC CCAAATCTCC AGTCACTCAC CAACCTGTTG TCCTCCAATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TCTTCCTCTG CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCAG GATCATCAAC AACCAGCACC GGACCATGCA AAACCTGCAC AACTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTACGGATGG AACTGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTCAGTTAT ATGGATGATA TGGTTTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATGCCGCT GTTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAACC	840
CTCACAAAAC AAAAAGATGG GGATATTCCC TTAACCTCAT GGGATATGTA ATTGGGAGCT	900
GGGGCACATT GCCACAGGAA CATATTGTAC AAAAAATCAA AATGTGGTTT AGGAAACTTC	960
CTGTAAACAG GCCTATTGAT TGGAAAGTAT GTCAACGAAT TGTGGGTCTT TTGGGGTTTG	1020
CCGCCCCCTT CACGCAATGT GGATATCCTG CTTTAATGCC TTTATATGCA TGTATACAAG	1080
CAAAACAGGC TTTTACTTTC TCGCCAACTT ACAAGGCCCTT TCTAACTAAA CAGTATCTGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCAG GTCTGTGCCA AGTGTTTGCT GACGCAACCC	1200
CCACTGGTTG GGGCTTGGCC ATAGGCCATC AGCGCATGCG TGGAACTTT GTGTCTCCTC	1260

TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTTTTGC	TCGCAGCCGG	TCTGGGGCAA	1320
AACTCATCGG	GACTGACAAT	TCTGTCGTGC	TCTCCCGCAA	GTATACATCA	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTTGTTTAC	GTCCCGTCGG	1440
CGTGAAATCC	CGCGGACGAC	CCTTCCCGGG	GCCGCTTGGG	GCTCTACCGC	CCGCTTCTCC	1500
GCCTGTTGTA	CCGACCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGACTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CACGGGAACC	TGCCCAAGGT	CTTGCCATAAG	AGGACTCTTG	GACTTTCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	GTGTTTAATG	AGTGGGAGGA	1740
GTTGGGGGAG	GAGGTTAGGT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
GTGTTACCA	GCACCATGCA	ACTTTTTTCAC	CTCTGCCTAA	TCATCTCATG	TTCATGTCTT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTGGG	GCATGGACAT	TGACCCGTAT	1920
AAAGAATTTG	GAGCTTCTGT	GGAGTTACTC	TCTTTTTTGC	CTTCTGACTT	CTTTCCGTGC	1980
GTGCGAGATC	TCCTCGACAC	CGCCTCTGCT	TTGTATCGGG	AGGCCTTAGA	GTCTCCGGAA	2040
CATTGTTTAC	CTCACCATAC	GGCACTCAGG	CAAGCTATTC	TGTGTTGGGG	TGAGTTAATG	2100
AATCTAGCCA	CCTGGGTGGG	AAGTAATTTG	GAAGATCCGG	CATCCAGGGA	ATTAGTAGTC	2160
AGCTATGTCA	ACGTTAATAT	GGGCCTAAAA	ATCAGACAAC	TATTGTGGTT	TCACATTTCC	2220
TGTCTTACTT	TTGGGAGAGA	AACTGTTCTT	GAATATTTGG	TGTCTTTTGG	AGTGTGGATT	2280
CGCACTCCTC	CTGCATATAG	ACCACCAAAT	GCCCCTATCT	TATCAACACT	TCCGGAAACT	2340
ACTGTTGTTA	GACGAAGAGG	CAGGTCCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGGTCTCAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCGGG	AATCTCAATG	TTAGTATTCC	2460
TTGGACACAT	AAGGTGGGAA	ACTTTACGGG	GCTTTATTCT	TCTACGGTAC	CTTGCTTTAA	2520
TCCTAAATGG	CAAACCTCCT	CTTTTCCTGA	CATTCATTTG	CAGGAGGACA	TTGTTGATAG	2580
ATGTAAGCAA	TTTGTGGGGC	CCCTTACAGT	AAATGAAAAC	AGGAGACTAA	AATTAATTAT	2640
GCCCGCTAGG	TTTTATCCCA	ATGTTACTAA	ATATTTGCCC	TTAGATAAAG	GGATCAAACC	2700
GTATTATCCA	GAGTATGTAG	TTAATCATT	CTTCCAGACG	CGACATTATT	TACACACTCT	2760
TTGGAAGGCG	GGGATCTTAT	ATAAAAGAGA	GTCCACACGT	AGCGCCTCAT	TTTGCGGGTC	2820
ACCATATTCT	TGGGAACAAG	ATCTACAGCA	TGGGAGGTTG	GTCTTCCAAA	CCTCGAAAAG	2880
GCATGGGGAC	AAATCTTTCT	GTCCCCAATC	CTCTGGGATT	CTTCCCCGAT	CATCAGTTGG	2940
ACCCTGCATT	CAAAGCCAAC	TCAGAAAATC	CAGATTGGGA	CCTCAACCCG	AACAAGGACA	3000
ACTGGCCGGA	CGCCAACAAG	GTGGGAGTGG	GAGCATTCGG	GCCAGGGTTC	ACCCCTCCCC	3060
ATGGGGGACT	GTTGGGGTGG	AGCCCTCAGG	CTCAGGGCCT	ACTCACAAC	GTGCCAGCAG	3120
CTCCTCCTCC	TGCCTCCACC	AATCGGCAGT	CAGGAAGGCA	GCCTACTCCC	TTATCCCCAC	3180
CTCTAAGGGA	CACTCATCCT	CAGGCCATGC	AGTGG			3215

(2) INFORMATION FOR SEQ ID NO: 288:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3213 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

AACTCCACCA CATTTCACCA AGTCCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTTCCT	60
CCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTGCGA CTA CTG CCTC ACCCATATCG	120
TCAATCTCCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAGCACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC CACCAGCACG GGACCATGCA AGACCTGCAC GATTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCTTGTGTC TGTACAAAAC CTTCCGACGG AAAC TGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGGG GGCCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCTG GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTTGTC TTTGGGTATA CATTGAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGCAGTT	900
GGGGTACTTT ACCGCAAGAA CATATTGTAC TAAAAATCAA GCAATGTTTT CGGAAACTGC	960
CTGTAAATAG ACCTATTGAC TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCTTT TACACAATGT GGCTATCCTG CCTTAATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACCTTC TCGCCAACTT ACAAGGCCTT TCTGTGTAAA CAATATCTGC	1140
ACCTTTACCC CGTTGCCCCG CGAACGGCTC TCTGCCAAGT ATTTGCTGAC GCAACCCCCA	1200
CTGGATGGGG CTTGGCCATA GGCCATCGGC GCATGCGTGG AACCTTTGTG GCTCCTCTGC	1260
CGATCCATAC TGC GGAACTC CTAGCAGCTT GTTTTGCTCG CAGCCGGTCT GGAGCGAAAC	1320
TCATCGGGAC TGACAACTCG GTTGTCTCT CTCCGAAATA CACCTCATTC CCATGGCTGC	1380
TCGGGTGTGC TGCCAACTGG ATCCTGCGCG GGACGTACTT TGTTTACGTC CCGTCGGCGC	1440
TGAATCCCGC GGACGACCCG TCTCGCGGCC GTTTGGGCCT CATCCGTCCC CTTCTTCATC	1500

TGCGGTTCCG	GCCGACCACG	GGGCGCACCT	CTCTTTACGC	GGTCTCCCCG	TCTGTGCCTT	1560
CTCATCTGCC	GGACCGTGTG	CACCTTCGCTT	CACCTCTGCA	CGTCGCATGG	AGACCACCGT	1620
GAACGCCGAT	CAGGTCTTGC	CCAAGGTCTT	ACATAAGAGG	ACTCTTGGAC	TCTCAGCAAT	1680
GTCAACGTCC	GACCTTGAGG	CATACTTCAA	AGACTGCTTG	TTTAAAGACT	GGGAGGACTT	1740
GGGGGAGGAG	ATTAGGTTAA	TGATCTTTGT	ACTAGGAGGC	TGTAGGCATA	AATTGGTCTG	1800
TTCACCAGCA	CCATGCAACT	TTTTTCACCT	CTGCCTAATC	ATCTCATGTT	CATGTCCTAC	1860
TGTTACAGCC	TCCAAGCTGT	GCCTTGGGTG	GCTTTGGGGC	ATGGACATTG	ACCCGTATAA	1920
AGAATTTGGA	GCTTCTGTGG	AGTTACTCTC	TTTTTTGCCT	TCTGATTCTT	TTCCTTCCAT	1980
TCGAGATCTC	CTCGACACCG	CCTCTGCTCT	GTATAGGGAG	GCCTTAGAGT	CTCCGGAACA	2040
TTGTTACCT	CATCATAACG	CACCTAGGCA	AGCTATTCTG	TGTTGGGGTG	AGTTGATGAA	2100
TCTGGCCACC	TGGGTGGGAA	GTAATTTGGA	AGACCCAGCA	TCCAGGGAAC	TAGTAGTCAG	2160
CTATGTCAAT	GTTAATATGG	GCCTAAAAAT	CAGACAATA	TTGTGGTTTC	ACATTTCCCTG	2220
CCTTACTTTT	GGAAGAGAAA	CTGTTTTGGA	GTATTTGGTA	TCTTTTGGAG	TGTGGATTCTG	2280
CACTCCTCCC	GCTTACAGAC	CACCAAATGC	CCCTATCTTA	TCAACACTTC	CGGAAACTAC	2340
TGTTGTTAGA	CGACGAGGCA	GGTCCCCTAG	AAGAAGAACT	CCCTCGCCTC	GCAGACGAAG	2400
ATCTGAATCG	CCGCGTCGCA	GAAGATCTCA	ATCTCGGGAA	TCTCAATGTT	AGTATCCCTT	2460
GGACTCATAA	GGTGGGAAAC	TTTACTGGGC	TTTATCTCTC	TACTGTACCT	GTCTTTAATC	2520
CTGAGTGGCA	AACTCCCTCC	TTTCTCACA	TTTATTACCA	GGAGGACATT	ATTAATAGAT	2580
GTCAACAATA	TGTGGGCCCT	CTTACAGTTA	ATGAAAAAAG	GAGATTAAAA	TTAATTATGC	2640
CTGCTAGGTT	TTATCCTAAA	CTTACCAAAT	ATTTGCCCTT	GGATAAAGGC	ATTAAACCTT	2700
ATTATCCTGA	ACATGCAGTT	AATCATTACT	TCAAACTAG	GCATTATTTA	CATACTCTGT	2760
GGAAGGCGGG	CATTCTATAT	AAGAGAGAAA	CTACACGCAG	CGCCTCATTT	TGTGGGTCAC	2820
CATATTCTTG	GGAACAAGAG	CTACAGCATG	GGAGGTTGGT	CTTCCAAACC	TCGACAAGGC	2880
ATGGGGACGA	ATCTTTCTGT	TCCCAATCCT	CTGGGATTCT	TTCCCGATCA	CCAGTTGGAC	2940
CCTGCGTTTC	GAGCCAACTC	AAACAATCCA	GATTGGGACT	TCAACCCCAA	CAAGGATCGT	3000
TGGCCAGAGG	CAAATCAGGT	AGGAGCGGGA	GCATTGCGGC	CAGGGTACCC	CCCACCACAC	3060
GGCGGTCTTT	TGGGGTGGAG	CCCTCAGGCT	CAGGGCATAT	TGACAACCGT	GCCAGCAGCA	3120
CCTCCTCCTG	CCTCCACCAA	TCGGCAGTCA	GGAAGACAGC	CTACTCCCAT	CTCTCCACCT	3180
CTAAGAGACA	GTCATCCTCA	GGCCATGCAG	TGG			3213

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AACTCCACCA CATTTCACCA AGTCCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTTCCT	60
CCTGGTGGCT CCAGTTCGG AACAGTAAAC CCTGTTCCGA CTA CTGCCTC ACCCATATCG	120
TCAATCTCCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAGCACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC CACCAGCAGG GGACCATGCA AGACCTGCAC GATTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCTTGTGTC TGTACAAAAC CTCGGGACGG AACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGGG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCTG GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAAGTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTTGTG TTTGGGTATA CATTTGAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAAGTTTCT GGGATATGTA ATTGGCAGTT	900
GGGGTACTTT ACCGCAAGAA CATATTGTAC TAAAAATCAA GCAATGTTTT CGGAAACTGC	960
CTGTAAATAG ACCTATTGAC TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCTTT TACACAATGT GGCTATCCTG CCTTAATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACTTTC TCGCCAACCT ACAAGGCCTT TCTGTGTAAG CAATATCTGC	1140
ACCTTTACCC CGTTGCCCCG CGAACGGCTC TCTGCCAAGT ATTTGCTGAC GCAACCCCCA	1200
CTGGATGGGG CTGCGCCATA GGCCATCGGC GCATGCGTGG AACCTTTGTG GCTCCTCTGC	1260
CGATCCATAC TGCAGAACTC CTAGCAGCTT GTTTTGCTCG CAGCCGGTCT GGAGCGAAAC	1320
TCATCGGGAC TGACAACTCG GTTGTTCTCT CTCGGAAATA CACCTCATTC CCATGGCTGC	1380
TCGGGTGTGC TGCCAACTGG ATCCTGCGCG GGACGTACTT TGTTTACGTC CCGTCGGCGC	1440
TGAATCCCGC GGACGACCCG TCTCGCGGCC GTTTGGGCCT CATCCGTCCC CTTCTTCATC	1500
TGCGGTTCGG GCCGACCACG GGGCGCACCT CTCTTTACGC GGTCTCCCCG TCTGTGCCTT	1560
CTCATCTGCC GGACCGTGTG CACTTCGCTT CACCTCTGCA CGTCGCATGG AGACCACCGT	1620
GAACGCCGAT CAGGTCTTGC CCAAGGTCTT ACATAAGAGG ACTCTTGGAC TCTCAGCAAT	1680

GTCAACGTCC GACCTTGAGG CATACTTCAA AGACTGCTTG TTAAAGACT GGGAGGACTT	1740
GGGGGAGGAG ATTAGGTAA TGATCTTGT ACTAGGAGGC TGTAGGCATA AATTGGTCTG	1800
TTCACCAGCA CCATGCAACT TTTTTCACCT CTGCCTAATC ATCTCATGTT CATGTCCTAC	1860
TGTTACGCC TCCAAGCTGT GCCTTGGGTG GCTTTGGGGC ATGGACATTG ACCCGTATAA	1920
AGAATTTGGA GCTTCTGTGG AGTTACTCTC TTTTTTGCCT TCTGATTTCT TTCCTTCCAT	1980
TCGAGATCTC CTCGACACCG CCTCTGCTCT GTATAGGGAG GCCTTAGAGT CTCCGGAACA	2040
TTGTTACCT CATCATACAG CACTCAGGCA AGCTATTCTG TGTTGGGGTG AGTTGATGAA	2100
TCTGGCCACC TGGGTGGGAA GTAATTTGGA AGACCCAGCA TCCAGGGAAC TAGTAGTCAG	2160
CTATGTCAAT GTTAATATGG GCCTAAAAAT CAGACAACTA TTGTGGTTTC ACATTTCCTG	2220
CCTTACTTTT GGAAGAGAAA CTGTTTTGGA GTATTTGGTA TCTTTTGGAG TGTGGATTCTG	2280
CACTCCTCCC GCTTACAGAC CACCAAATGC CCTTATCTTA TCAACACTTC CGGAACTAC	2340
TGTTGTTAGA CGACGAGGCA GGTCCCCTAG AAGAAGAACT CCCTCGCCTC GCAGACGAAG	2400
ATCTGAATCG CCGCTCGCA GAAGATCTCA ATCTCGGGAA TCTCAATGTT AGTATCCCTT	2460
GGACTCATAA GGTGGGAAAC TTTACTGGGC TTTATTCTTC TACTGTACCT GTCTTTAATC	2520
CTGAGTGGCA AACTCCCTCC TTTCTCACA TTCATTTACA GGAGGACATT ATTAATAGAT	2580
GTCAACAATA TGTGGGCCCT CTTACAGTTA ATGAAAAAG GAGATTAAAA TTAATTATGC	2640
CTGCTAGGTT TTATCCTAAA CTTACCAAAT ATTTGCCCTT GGATAAAGGC ATTAAACCTT	2700
ATTATCCTGA ACATGCAGTT AATCATTACT TCAAACTAG GCATTATTTA CATACTCTGT	2760
GGAAGGCGGG CATTCTATAT AAGAGAGAAA CTACACGCAG CGCCTCATTT TGTGGGTCAC	2820
CATATTCTTG GGAACAAGAG CTACAGCATG GGAGGTGGT CTTCCAAACC TCGACAAGGC	2880
ATGGGGACGA ATCTTTCTGT TCCCAATCCT CTGGGATTCT TTCCCGATCA CCAGTTGGAC	2940
CCTGCGTTTG GAGCCAACTC AAACAATCCA GATTGGGACT TCAACCCCAA CAAGGATCGT	3000
TGGCCAGAGG CAAATCAGGT AGGAGCGGGA GCATTGGGC CAGGGTACCC CCCACCACAC	3060
GGCGGTCTTT TGGGGTGGAG CCCTCAGGCT CAGGGCATAT TGACAACCGT GCCAGCAGCA	3120
CCTCCTCCTG CCTCCACCAA TCGGCAGTCA GGAAGACAGC CTACTCCCAT CTCTCCACCT	3180
CTAAGAGACA GTCATCCTCA GGCCATGCAG TGG	3213

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

AACTCCACAA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTTCCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTA CTGTCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAGCACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTCTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCTTGTTGC TGTACAAAAC CTTCCGACGG AACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTTCGCAGG GCTTTCCCCC	720
ACTGTTTGGC TTTTCAATTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTTGTC TTTGGGTATA CATTTGAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGAAGTT	900
GGGGTACTTT ACCACAGGAA CATATTGTAT TAAAACTCAA GCAATGTTTT CGAAAACTGC	960
CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCCTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTGTATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACTTTC TCGCCAACTT ATAAGGCCTT TCTGTGTCAA CAATACCTGC	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGATG GGGCTTGCC ATAGGCCATC GCGCATGCG TGGAACCTTT GTGGTTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTTGC TCGCGACCGG TCTGGAGCAA	1320
AACTTATCGG GACTGACAAC TCGGTTGTCC TCTCTCGGAA ATACACCTCC TTCCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTTGGG CCTCTACCGT CCCTTGCTTT	1500
CTCTGCCGTT CCAGCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGGC CACCAGGTCT TGCCCAAGCT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
AATGTCAACA ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGGT TAAAGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTTTAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860

ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTTG GAGCTTCTGT GGAGTTACTC TCTTTTTTGC CTTCTGACTT CTTTCCTTCT	1980
ATTCGAGATC TCCTCGACAC CGCCTCTGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTTAC CTCACCATAC AGCACTCAGG CAAGCTATTC TGTGTTGGGG TGAGTTGATG	2100
AATTTGGCCA CCTGGGTGGG AAGTAATTTG GAAGACCCAG CATCCAGGGA ATTAGTAGTC	2160
AGCTATGTCA ATGTTAATAT GGGCCTAAAA ATCAGACAAC TATTGTGGTT TCATATTTCC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAGTATTTGG TGTCTTTTGG AGTGTGGATT	2280
CGCACTCCTC CCGCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCCTTAA	2520
TCCTGAGTCC CAAACTCCCT CTTTCCTAA CATTCAATTA CAGGAGGACA TTATTAATAG	2580
ATGTCAACAA TATGTGGGCC CTCTTACAGT TAATGAAAAA AGGAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCCC TTGGATAAAG GCATTAAACC	2700
TTATTATCCT GAACATGCAG TTAATCATT CTTCAAACT AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATTCTAT ATAAAAGAGA AACTACACGC AGCGCTTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACGGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGGAC GAATCTTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940
ACCCTGCGTT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAGGATC	3000
ACTGGCCAGA GGCAATCAAG GTAGGAGCGG GAGACTTCGG GCCAGGGTTC ACCCCACCAC	3060
ACGGCGGTCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA GTGCCAGCAG	3120
CGCCTCCTCC TGTTTCCACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:



AACTCCACAA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTTCCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTA CTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAGCACAAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GACTACCAAG GTATGTGCCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCTGCT	540
CAAGGAACCT CTATGTTTCC CTCTTGTTGG TGTACAAAAC CTTCCGACGG AACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTCGCAGG GCTTTCCCCC	720
ACTGTTTGGC TTTTCACTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTTGT TTTGGGTATA CATTTGAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGAAGTT	900
GGGGTACTTT ACCACAGGAA CATATTGTAT TAAAACTCAA GCAATGTTTT CGGAAACTGC	960
CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCCTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACTTTC TCGCCAACTT ATAAGGCCTT TCTGTGTCAA CAATACCTGC	1140
ACCTTTACCC CGTTGCCCCG CAACGGTCAG GTCTCTGCCA AGTGTTTGGT GACGCAACCC	1200
CCACTGGATG GGGCTTGGCC ATAGGCCATC GGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AACTTATCGG GACTGACAAC TCTGTTGTCC TCTCTCGGAA ATACACCTCC TTCCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTTGGG CCTCTACCGT CCCCTTCTTC	1500
ATCTGCCGTT CCAGCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTACCTCT GCACGTGCA TGGAGACCAC	1620
CGTGAACGCC CACCAGGTCT TGCCTAAGCT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTTG GAGCTTCTGT GGAGTTACTC TCTTTTTTGC CTTCTGACTT CTTTCCTTCT	1980
ATTGAGATC TCCTCGACAC CGCCTCTGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040

CATTGTTCAC CTCACCATAC AGCACTCAGG CAAGCTATCC TGTGTTGGGG TGAGTTGATG	2100
AATTTGGCCA CCTGGGTGGG AAGTAATTTG GAAGACCCAG CATCCAGGGA ATTAGTAGTC	2160
AGCTATGTCA ATGTTAATAT GGGCCTAAAA ATCAGACAAC TATTGTGGTT TCACATTTC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAGTATTTGG TGTCTTTTGG AGTGTGGATT	2280
CGCACTCCTC CCGCTTACAG ACCACCAAAT GCCCCTATCT TATCAAACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTTAA	2520
TCCTGAGTGC CAAACTCCCT CCTTTCCTAA CATTCAATTA CAAGAGGATA TTATTAATAG	2580
ATGTCAACAA TATGTGGGCC CTCTTACAGT TAATGAAAAA AGGAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCCC TTGGATAAAG GCATTAAACC	2700
TTATTATCCT GAACATGCAG TTAATCATT CTTCAAAAC AGGCATTATT TACATACGCT	2760
GTGGAAGGCT GGCATTCTAT ATAAAAGAGA AACTACACGC AGCGCTTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGGAC GAATCTTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940
ACCCTGCGTT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAGGATC	3000
ACTGGCCAGA CGGAATCAAG GTAGGAGCGG GAGACTTCGG GCCAGGGTTC ACCCCACCAC	3060
ACGGCGGTCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT CTTGACAACA GTGCCAGCAG	3120
CTCCTCCTCC TGCCTCCACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 292:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

AACTCCACAA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAGCACAAC ATCAGGATTC	180

CTAGGACCCC	TGCTCGTGTT	ACAGGCGGGG	TTTTTCTTGT	TGACAAGAAT	CCTCACAATA	240
CCACAGAGTC	TAGACTCGTG	GTGGACTTCT	CTCAATTTTC	TAGGGGGAGC	ACCCACGTGT	300
CCTGGCCAAA	ATTGCGAGTC	CCCAACCTCC	AATCACTCAC	CAACCTCTTG	TCCTCCAAC	360
TGTCCTGGCT	ATCGCTGGAT	GTGTCTGCGG	CGTTTTATCA	TATTCCTCTT	CATCCTGCTG	420
CTATGCCTCA	TCTTCTTGTT	GGTTCTTCTG	GACTACCAAG	GTATGTTGCC	CGTTTGTCTT	480
CTACTTCCAG	GAACATCAAC	TACCAGCAGG	GGACCATGCA	GAACCTGCAC	GATTCCTGCT	540
CAAGGAACCT	CTATGTTTCC	CTCTTGTTGC	TGTACAAAAC	CTTCGGACGG	AAACTGCACT	600
TGTATTCCCA	TCCCATCATC	CTGGGCTTTC	GCAAGATTCC	TATGGGAGTG	GGCCTCAGTC	660
CGTTTCTCCT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTTCACT	GGTTCGTAGG	GCTTTCCCCC	720
ACTGTTTGGC	TTTCAGCTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAACATC	780
TTGAGTCCCT	TTTTACCTCT	ATTACCAATT	TTCTTTTGTG	TTTGGGTATA	CATTTGAACC	840
CTAATAAAAC	CAAACGTTGG	GGCTACTCCC	TTAACTTCAT	GGGATATGTA	ATTGGAAGTT	900
GGGGTACTTT	ACCGCAGGAA	CATATTGTAC	AAAAACTCAA	GCAATGTTTT	CGAAAATTGC	960
CTGTAAATAG	ACCTATTGAT	TGGAAAGTAT	GTCAAAGAAT	TGTGGGTCTT	TTGGGCTTTG	1020
CTGCCCCCTT	TACACAATGT	GGCTATCCTG	CCTTGATGCC	TTTATATGCA	TGTATACAAT	1080
CTAAGCAGGC	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTGTGTAAA	CAATATCTAA	1140
ACCTTTACCC	CGTTGCCCGG	CAACGGTCAG	GTCTCTGCCA	AGTGTTTGCT	GACGCAACCC	1200
CCACGGGTTG	GGGCTTGCC	ATAGGCCATC	GGCGCATGCG	TGGAACCTTT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCAG	CTTGTTTTGC	TCGCAGCCGG	TCTGGAGCGA	1320
AACTTATCGG	AACCGACAAC	TCAGTTGTCC	TCTCTCGGAA	ATACACCTCC	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTTGTCTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCGTCTCGGG	GCCGTTTGGG	CCTCTACCGT	CCCCTTCTTC	1500
ATCTGCCGTT	CCGGCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTAGCA	TGGAGACCAC	1620
CGTGAACGCC	CACCAGGTCT	TGCCCCAAGT	CTTACACAAG	AGGACTCTTG	GACTCTCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	TTGTTTAAAG	ACTGGGAGGA	1740
GTTGGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGTTACCA	GCACCATGCA	ACTTTTTCCC	CTCTGCCTAA	TCATCTCATG	TTCATGTCTT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTGGG	GCAATGGACAT	TGACCCGTAT	1920
AAAGAATTTG	GAGCTTCTGT	GGAGTTACTC	TCTTTTTTGC	CTTCTGACTT	CTTTCCTTCT	1980
ATTGAGATC	TCCTCGACAC	CGCCTCTGCT	CTGTATCGGG	AGGCCTTAGA	GTCTCCGGAA	2040
CATTGTTTAC	CTCACCATAC	AGCACTCAGG	CAAGCTATTC	TGTGTTGGGG	TGAGTTGATG	2100
AATCTGGCCA	CCTGGGTGGG	AAGTAATTTG	GAAGACCCAG	CATCCAGGGA	ATTAGTAGTC	2160
AGCTATGTCA	ATGTTAATAT	GGGCCTAAAA	ATTAGACAAC	TATTGTGGTT	TCACATTTCC	2220

TGCCTTACTT TTGGAAGAGA AACTGTCCTT GAGTATTTGG TGTCTTTTGG AGTGTGGATT	2280
CGCACTCCTC CCGCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCCT AGAAGAAGAA CTCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTTAA	2520
TCCTGATTGG AAAACTCCCT CTTTCTCTCA CATTCAATTA CAGGAGGACA TTATTAATAG	2580
ATGTCAACAA TATGTGGGCC CTCTGACAGT TAATGAAAAA AGGAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCCC TTGGACAAAG GCATTAAACC	2700
GTATTATCCT GAATATGCAG TTAATCATTA CTTCAAAACT AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATTCTAT ATAAGAGAGA AACTACACGC AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGGAC GAATCTTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940
ACCCTGCGTT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAGGATC	3000
ACTGGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTG TCCAGGGTTC ACCCCACCAC	3060
ACGGAGGCCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA CTGCCAGCAG	3120
CACCTCCTCC TGCTCCACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

AATCCACAA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAACACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360

TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC CACCAGCACG GGGCCATGCA AGACCTGCAC GATTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCTTGTTGC TGTACAAAAC CTTCGGACGG AAACCTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCAGT GGTTCTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGAAGTT	900
GGGGTACTTT ACCGCAGGAA CATATTGTAC TAAAACTCAA GCAATGTTTT CGAAAATTGC	960
CTGTAAATAG CCCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCCTT TACACAATGC GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACCTTC TCGCCAACTT ATAAGGCCTT TCTGTGTAAA CAATATCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTTTGCT GACGCAACCC	1200
CCACTGGATG GGGCTTGCC ATAGGCCATC GCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTTGC TCGCAGCCGG TCTGGAGCGA	1320
AACTTATCGG AACCGACAAC TCTGTTGTCC TCTCTCGGAA ATACACCTCC TTTCCATGGC	1380
TGCTAGGGTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTCCCGTCGG	1440
CGCTGAATCC CCGGACGAC CCGTCTCGGG GCCGTTTGGG GCTCTACCGT CCCCTTCTTC	1500
TTCTGCCGTT CCGGCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCAGGTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
CATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT GTGTTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGGT TAAAGGTCTT TGTAAGTAGG GGCTGTAGGC ATAACCTTTT	1800
CACCTCTGCC TAATCATCTC ATGTTTCATG CTTACTGTTT AAGCCTCCAA GCTGTGCCTT	1860
GGGTGGCTTT GGGGCATGGA CATTGACCCG TATAAAGAAT TTGGAGCATC TGTGGAGTTA	1920
CTCTCTTTTT TGCCTTCTGA CTTCTTTCCG TCTATTCGAG ATCTCCTTGA CACCGCCTCT	1980
GCTCTGTATC GGGAGGCCTT AGAGTCTCCG GAACATTGTT CACCTCACCA TACAGCACTC	2040
AGGCAAGCTA TTCTGTGTTG GGGTGAGTTA ATGAATCTGG CCACCTGGGT GGGAAAGTAAT	2100
TTGGAAGACC CAGCATCCAG GGAATTAGTA GTCAGCTATG TCAATGTAA TATGGGCCTA	2160
AAAATCAGAC AACTATTGTG GTTTCACATT TCCTGCCTTA CTTTGGGAAG AGAAACTGTT	2220
TTGGAGTATT TGGTATCTTT TGGAGTGTGG ATTGCACTC CTCCCGCTTA CAGACCACCA	2280
AATGCCCTTA TCTTATCAAC ACTTCCGGAA ACTACTGTTG TTAGACGACG AGGCAGGTCC	2340
CCTAGAAGAA GAACTCCCTC GCCTCGCAGA CGAAGGTCTC AATCGCCGCG TCGCAGAAGA	2400

TCTCAATCTC GGAATCTCA ATGTTAGTAT CCCTTGGACT CATAAGGTGG GAAACTTTAC	2460
TGGGCTTTAT TCTTCTACTG TACCTGTCTT TAATCCCGAG TGGCAAACCTC CCTCCTTTCC	2520
TCACATTCAT TTACAGGAGG ACATTATTAA TAGATGTCAA CAATATGTGG GCCCTCTTAC	2580
GGTTAATGAA AAAAGGAGAT TAAAATTAAT TATGCCTGCT AGGTTCTATC CTAACCTTAC	2640
TAAATATTTG CCCTTAGACA AAGGCATTAA ACCGTATTAT CCTGAACATG CAGTTAATCA	2700
TTACTTCAAA ACTAGGCATT ATTTACATAC TCTGTGGAAG GCTGGCATTG TATATAAGAG	2760
AGAAACTACA CGCAGCGCCT CATTTTGTGG GTCACCATAT TCTTGGGAAC AAGAGCTACA	2820
GCATGGGAGG TTGGTCTTCC AAACCTCGAC AAGGCATGGG GACGAATCTT TCTGTTCCCA	2880
ATCCTCTGGG ATTCTTTCCC GATCACCAGT TGGACCCTGC GTTCGGAGCC AACTCAAACA	2940
ATCCAGATTG GGAATTCAAC CCCAACAGG ATCAATGGCC AGAGGCAAAT CAGGTAGGAG	3000
CGGGAGCATT CGGGCCAGGG TTCACCCAC CACACGGCGG TCTTTTGGGG TGGAGCCCTC	3060
AGGCTCAGGG CATATTGACA ACAGTGCCAG CAGCACCTCC TCCTGCCTCC ACCAATCGGC	3120
AGTCAGGAAG ACAGCCTACT CCCATCTCTC CACCTCTAAG AGACAGTCAT CCTCAGGCCA	3180
TGCAGTGG	3188

(2) INFORMATION FOR SEQ ID NO: 294:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3214 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AACTCCACAA CATTCCACCA AGCTCTGCTA GACCCAGAG TGAGGGGCCT ATACTTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTAAAC CCTGTTCCGA CTA CTGCCTC ACCCATATCG	120
TCAATCTCCT CGAGGACTGG GGACCTGCA CCGAACATGG AGAACACAAC ATCAGGATTG	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC TACCAGCAGG GGACCATGCA AGACCTGCAC GATTCCTGCT	540

CAAGGAACCT CTATGTTTCC CTCTTGTTGC TGTACAAAAC CTTCCGGACGG AACTGCACT	600
TGTATTTCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGGG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGATGTT	900
GGGGTACTTT ACCGCAAGAA CATATTGTAC TAAAAATCAA GCAATGTTTT CGAAAACTGC	960
CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAGAGACT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCCTT TACACAATGT GGCTATCCTG CCTTAATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACCTTC TCGCCAACCT ACAAGGCCTT TCTGTGTAAA CAATATCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGTGCT GACGCAACCC	1200
CCACTGGATG GGGCTTGGCT ATCGGCCATA GCCGCATGCG CGGACCTTTG TGGCTCCTCT	1260
GCCGATCCAT ACTGCGGAAC TCCTAGCAGC TTGTTTTGCT CGCAGGCGGT CTGGAGCGAA	1320
ACTTATCGGC ACCGACAACT CTGTTGTCTT CTCTCGGAAA TACACCTCCT TTCCATGGCT	1380
GCTAGGGTGT GCTGCCAACT GGATCCTGCG CGGGACGTCC TTTGTCTACG TCCCGTCGGC	1440
GCTGAATCCC GCGGACGACC CGTCTCGGGG CCGTTTGGGA CTCTACCGTC CCCTTCTTCA	1500
TCTGCCGTTT CGGCCGACCA CGGGGCGCAC CTCTCTTTAC GCGGTCTTTT TGTCTGTGCC	1560
TTCTCATCTG CCGGTCCGTG TGCACCTCGC TTCACCTCTG CACGTGCGAT GGAGACCACC	1620
GTGAACGCCC ACCAGGTCTT GCCCAAGGTC TTACATAAGA GGAATCTTGG ACTCTCAGCG	1680
ATGTCAACGA CCGACCTTGA GGCATACTTC AAAGACTGTT TGTTTAAGGA CTGGGAGGAG	1740
TTGGGGGAGG AGATTAGGTT AAAGGTCTTT GTACTAGGAG GCTGTAGGCA TAAATTGGTC	1800
TGTTCAACAG CACCATGCAA CTTTTTCACC TCTGCCTAAT CATCTCATGT TCATGTCCTA	1860
CTGTTCAAGC CTCCAAGCTG TGCCTTGGGT GGCTTTGGGG CATGGACATT GACCCGTATA	1920
AAGAATTTGG AGCTTCTGTG GAGTTACTCT CTTTTTTGCC TTCTGACTTC TTTCCTCTA	1980
TTCGAGATCT CCTCGACACC GCCTCAGCTC TATATCGGGA GGCCTTAGAG TCTCCGGAAC	2040
ATTGTTCTCC TCATCATACA GCACTCAGGC AAGCTATTCT GTGTTGGGGT GAGTTGATGA	2100
ATCTGGCCAC CTGGGTGGGA AGTAATTTGG AAGACCCAGC ATCCAGGGAA TTAGTAGTCA	2160
GCTATGTCAA TGTTAATATG GGCCTAAAAA TCAGACAACT ACTGTGGTTT CACATTTCTT	2220
GTCTTACTTT TGGAAGAGAA ACTGTTCTTG AGTATTTGGT GTCTTTTGGA GTGTGGATTC	2280
GCACTCCTCC TGCTTACAGA CCACCAAATG CCCCTATCTT ATCAACACTT CCGGAAACTA	2340
CTGTTGTTAG ACGACGAGGC AGGTCCCCTA GAAGAAGAAC TCCCTCGCCT CGCAGACGAA	2400
GGTCTCAATC GCCGCGTCGC AGAAGATCTC AATCTCGGGA ATCTCAATGT TAGTATCCCT	2460
TGGACTCATA AGGTGGGAAA CTTTACTGGG CTTTATTCTT CTAATGTACC TGTCTTTAAT	2520
CCTGAGTGGC AACTCCCTC CTTTCCTCAC ATTCATTTAC AGGAGGACAT TATTAATAGA	2580

TGCAACAAT ATGTGGGCCC TCTTACAGTT AATGAAAAA GGAGATTAAA ATTAATTATG	2640
CCTGCTAGGT TCTATCCTAA CCTTACCAA TATTTGCCAT TGGACAAAGG CATTAAACCA	2700
TATTATCCTG AACATGCAGT TAATCATTAC TTCAAACTA GGCATTATTT ACATACTCTG	2760
TGGAAGGCGG GCATTCTATA TAAGAGAGAA ACTACACGCA GTGCCTCATT CTGTGGGTCA	2820
CCATATTCTT GGGAACAAGA GCTACAGCAT GGGAGGTTGG TCTTCCAAAC CTCGACAAGG	2880
CATGGGGACG AATCTTTCTG TTCCCAATCC TCTGGGATTC TTTCCCGATC ACCAGTTGGA	2940
CCCTGCGTTC GGAGCCAACT CACACAATCC CGATTGGGAC TTCAACCCCA ACAAGGATCA	3000
TTGGCCAGAG GCAAATCAGG TAGGAGCGGG AGCATTCCGG CCAGGGTTCA CCCCACCACA	3060
CGGCGGTCTT TTGGGGTGA GCCCGCAGGC TCAGGGCGTA TTGACAACCG TGCCAGTAGC	3120
ACCTCCTCCT GCCTCCACCA ATCGGCAGTC AGGAAGACAG CCTACTCCA TCTCTCCACC	3180
TCTAAGAGAC AGTCATCCTC AGGCCATGCA GTGG	3214

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

AACTCCACAA CATTCCACCA AGCTCTGCTA GACCCAGAG TGAGGGGCCT ATACTTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAACACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TACACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGCAGC ACCCACGTGT	300
CTTGGCCAAA ATTGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGTT ATCGTTGGAT GTGTCTGCGG CGTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTACCAAG GTATGTTGTC TGTTTGTCTT	480
CTACTTCCAA GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCTTCTTGC TGTACAAAC CTTCGGACGG AAACCTGCACT	600
TGTATTCCCA TCCCATCATC TTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCGTAGG GCTTCCCCC	720
ACTGTTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780



TTGAGTCCCT	TTTTACCTCT	ATTACCAATT	TTCTTTTGTC	TTTGGGTATA	CATTTGAACC	840
CCAATAAAAC	CAAACGTTGG	GGCTATTCCC	TTAATTTTCAT	GGGATATGTA	ATTGGATGTT	900
GGGGTACTTT	ACCGCAAGAA	CATATTGTAC	TAAAAATCAA	GCAATGTTTT	CGAAAACTGC	960
CTGTAAATAG	ACCTATTGAT	TGGAAAGTAT	GTCAGAGAAT	TGTGGGTCTT	TTGGGCTTTG	1020
CTGCCCCTTT	TACACAATGT	GGCTATCCTG	CCTTGATGCC	TTTATATGCA	TGTATACAAT	1080
CTAAGCAAGC	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTGTGTAAA	CAATATCTGA	1140
ACCTTTACCC	CGTTGCCCGG	CAACGGTCAG	GTCTCTGCCA	AGTGTTCGCT	GACGCAACCC	1200
CCACTGGATG	GGGCTTGGCT	ATTGGCCATC	GCCGCATGCG	TGGAACCTTT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTGGCAG	CCTGTTTTGC	TCGCAGCCGG	TCTGGAGCAA	1320
AACTTATCGG	AACCGACAAC	TCTGTTGTCC	TCTCTCGGAA	ATACACCTCC	TTTCCATGGC	1380
TGCTCGGGTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTTGTCTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCGTCTCGGG	GCGGTTTGGG	CCTCTATCGT	CCCCTTCTTC	1500
ATCTACCGTT	CCGGCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCC	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CACCAGGTCT	TGCCCCAAGT	CTTACATAAG	AGCACTCTTG	GACTCTCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	TTGTTTAAGG	ACTGGGAGGA	1740
GTTGGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTACTGGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGTTACCA	GCACCATGCA	ACTTTTTCAC	CTCTGCCTAA	TCATCTCATG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTGGG	GCATGGACAT	TGAGCCGTAT	1920
AAAGAATTTG	GAGCTTCTGT	GGAGTTACTC	TCTTTTTTGC	CTTCTGACTT	CTTTCCTTCT	1980
ATTCGAGATC	TCCTCGACAC	CGCCTCAGCT	CTGTATCGGG	AGGCCTTAGA	GTCTCCGGAA	2040
CATTGCTCAC	CTCACCATAC	CGCACTCAGG	CAAGCTATTC	TGTGTTGGCG	TGAGTTGATG	2100
AATCTGGCCA	CCTGGGTGGG	AAGTAATTTG	GAAGACCCAG	CATCCAGGGA	ATTAGTAGTC	2160
AGCTATGTCA	ATGTTAATAT	CGGCCTAAAA	ATCAGACAAC	TACTGTGGTT	TCACATTTCC	2220
TGTCTTACTT	TTGGAAGAGA	AACTGTTCTT	GAGTATTTGG	TGTCTTTTGG	AGTGTGGATT	2280
CGCACTCCTC	CTGCTTACAG	ACCACCAAAT	GCCCCATCT	TATCAAACT	TCCGGAAACT	2340
ACTGTTGTTA	GACGACGAGG	CAGGTCCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGGTCTCAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCGGG	AATCTCAATG	TTAGTATCCC	2460
TTGGACTION	AAGGTGGGAA	ACTTTACTGG	GCTTTATCT	TCTACTGTAC	CTATCTTTAA	2520
TCCTGAGTGG	CAAACTCCCCT	CCTTTCCTCA	CATTCAATTA	CAGGAGGACA	TTATTAATAG	2580
ATGTCAACAA	TATGTGGGCC	CTCTTACAGT	TAATGAAAAA	AGGAGATTAA	AGTTAATTAT	2640
GCCTGCTAGG	TTCTATCCTA	ACCTTACCAA	ATATCTGCCC	TTGGACAAAG	GCATTAAACC	2700
ATATTATCCT	GAACATGCAG	TTAATCATT	CTTCAAACT	AGGCATTATT	TACATACTCT	2760

GTGGAAGGCG GGCATTCTAT ATAAGAGAGA AACTACGCGC AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGGAC GAATCTTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940
ACCCTGCGTT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAGGATC	3000
ACTGGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTCCG GCCAGGGTTC ACCCCACCAC	3060
ACGGCGGTCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA GTGCCAGTAG	3120
CACCTCCTCC TGCCTCCACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

AACTCCACAA CATTCCACCA AGCTGTGCTA GATCCAGAG TGAGGGGCCT ATATCTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTGAAC CCTGTTCCGA CTAAGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAACACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCAGTGT	300
CCTGGCCCAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC TACCAGCAGG GGACCATGCA AGACCTGCAC GATTCTGCT	540
CAAGGAACCT CTATGTTTCC CTCCTGTTGC TGTACAAAAC CTTCGGACGG AACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTTCACTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTTGT TTTGGGTATA CATTTGAACC	840
CTCATAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGAAGTT	900
GGGGTACTTT ACCACAGGAA CATATTGTAC TAAAAATCAA GCAATGTTTT CGGAAGCTGC	960

CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAAAGGAT TGTGGGTCTT TTGGCCTTTG	1020
CTGCCCCCTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACCTTC TCGCCAACTT ACAAGGCCTT TCTGTGTAAA CAATATCTGC	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTTTGCT GACGCAACCC	1200
CCACTGGATG GGGCTTGGCC ATTGGCCAAT CGGGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTTGC TCGCAGCCGG TCTGGAGCGA	1320
AACTTATCGG GACTGACAAC TCTGTTGTCC TCTCTCGGAA ATACACCTCC TTCCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTTGGG CCTCTACCGT CCCCTTCTTC	1500
ATCTGCCGTT CCGGCCGACC ACGGGGCGCG CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCAGGTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
GATGTCAACG ACCGACCTTG AGGCATATTT CAAAGACTGT TTGTTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGGT TAATGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTACCA GCACCATGCA ACTTTTTTAC CTCTGCCTAA TCATCTCCTG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTAGGG GCATGGACAT TGACACGTAT	1920
AAAGAATTTG GAGCTTCTGT GGAGTTACTC TCTTTTTTGC CTTCTGACTT CTTTCCTTCT	1980
ATTCGAGATC TCCTCGACAC CGCCTTTGCT CTGCATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTTAC CTCACCATAC AGCACTCAGG CAAGCTATTG TGTGTTGGGG TGAGTTGATG	2100
AATCTGGCCA CCTGGGTGGG AAGTAATTTG GAAGACCCAG CATCCAGGGA ATTGGTAGTC	2160
AGCTATGTCA ATGTTAATAT GGGCCTAAAA ATCAGACAAC TATTGTGGTT TCACATTTCC	2220
TGTCTTACTT TTGGAAGAGA AACGGTTCTT GAGTATTTGG TATCTGTTGG AGTGTGGATT	2280
CGCACTCCTC AAGCCTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTAAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACTGG TCTCTATTCT TCTACTGTAC CTGTCTTTAA	2520
TCCTGAGTGG CAAACTCCCT CCTTTCCTAA TATTCATTTA CAGGAGGATA TTATTAATAG	2580
ATGTCAACAA TATGTAGGCC CTCTTACAGT TAATGAAAAA AGGAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCCC TTGGATAAAG GTATTAAACC	2700
TTATTATCCT GAACATGCAG TTAATCATT TTTCAAACT AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATTCTAT ATAAGAGAGA AACTACACGT AGTGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGGAC GAATCTTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940

ACCCTGCATT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAAGGATC	3000
ATTGGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTGTT GCCAGGGTTC ACTCCACCAC	3060
ACGGCGGTCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA GTGCCAGCAG	3120
CGCCTCCTCC TGCCTCTACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

AATCCACAA CATTCCACCA AGCTGTGCTA GATCCCAGAG TGAGGGGCCT ATATCTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTGAAC CCTGTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAACACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCCAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC TACCAGCAGG GGACCATGCA AGACCTGCAC GATTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCCTGTTGC TGTACAAAAC CTTGGGACGG AAAGTGAAGT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTTCACTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTTGTC TTTGGGTATA CATTGAACC	840
CTCATAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGAAGTT	900
GGGGTACTTT ACCACAGGAA CATATTGTAC TAAAAATCAA GCAATGTTTT CGGAAGCTGC	960
CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAAAGGAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCCTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACCTTC TCGCCAACTT ACAAGGCCTT TCTGTGTAAA CAATATCTGC	1140

ACCTTTACCC	CGTTGCCCCG	CAACGGTCAG	GTCTCTGCCA	AGTGTGCT	GACGCAACCC	1200
CCACTGGATG	GGGCTTGGCC	ATTGGCCAAT	CGGGCATGCG	TGGAACCTTT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCAG	CTTGTTTTGC	TCGCAGCCGG	TCTGGAGCGA	1320
AACTTATCGG	GACTGACAAC	TCTGTTGTCC	TCTCTCGGAA	ATACACCTCC	TCCCCATGGC	1380
TGCTCGGGTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTTGTCTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCGTCTCGGG	GCCGTTTGGG	CCTCTACCGT	CCCCTTCTTC	1500
ATCTGCCGTT	CCGGCCGACC	ACGGGGCGCG	CCTCTCTTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGTCCGT	GTGCACTTCG	CTTCACCTCT	GCACGTGCGA	TGGAGACCAC	1620
CGTGAACGCC	CACCAGGTCT	TGCCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCTCAGC	1680
GATGTCAACG	ACCGACCTTG	AGGCATATTT	CAAAGACTGT	TTGTTTAAAG	ACTGGGAGGA	1740
GTTGGGGGAG	GAGATTAGGT	TAATGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGTTCACCA	GCACCATGCA	ACTTTTTTCAC	CTCTGCCTAA	TCATCTCCTG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTAGGG	GCATGGACAT	TGACACGTAT	1920
AAAGAATTTG	GAGCTTCTGT	GGAGTTACTC	TCTTTTTTGC	CTTCTGACTT	CTTTCCTTCT	1980
ATTCGAGATC	TCCTCGACAC	CGCCTTTGCT	CTGCATCGGG	AGGCCTTAGA	GTCTCCGGAA	2040
CATTGTTTAC	CTCACCATAC	AGCACTCAGG	CAAGCTATTG	TGTGTTGGGG	TGAGTTGATG	2100
AATCTGGCCA	CCTGGGTGGG	AAGTAATTTG	GAAGACCCAG	CATCCAGGGA	ATTGGTAGTC	2160
AGCTATGTCA	ATGTTAATAT	GGGCCTAAAA	ATCAGACAAC	TATTGTGGTT	TCACATTTC	2220
TGTCTTACTT	TTGGAAGAGA	AACGGTTCTT	GAGTATTTGG	TATCTGTTGG	AGTGTGGATT	2280
CGCACTCCTC	AAGCCTACAG	ACCACCAAAT	GCCCCATCT	TATCAACACT	TCCGGAAACT	2340
ACTGTTGTTA	GACGACGAGG	CAGGTCCCCT	AGAAGAAGAA	CTCCCTCGCG	TCGCAGACGA	2400
AGGTCTAAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCGGG	AATCTCAATG	TTAGTATCCC	2460
TTGGACTCAT	AAGGTGGGAA	ACTTTACTGG	TCTCTATTCT	TCTACTGTAC	CTGTCTTTAA	2520
TCCTGAGTGG	CAAACCTCCCT	CCTTTCCTAA	TATTCATTTA	CAGGAGGATA	TTATTAATAG	2580
ATGTCAACAA	TATGTAGGCC	CTCTTACAGT	TAATGAAAAA	AGGAGATTAA	AATTAATTAT	2640
GCCTGCTAGG	TTCTATCCTA	ACCTTACCAA	ATATTTGCCC	TTGGATAAAG	GTATTAAACC	2700
TTATTATCCT	GAACATGCAG	TTAATCATTA	TTTCAAAACT	AGGCATTATT	TACATACTCT	2760
GTGGAAGGCT	GGCATTCTAT	ATAAGAGAGA	AACTACACGT	AGTGCCTCAT	TTTGTGGGTC	2820
ACCATATTCT	TGGGAACAAG	AGCTACAGCA	TGGGAGGTTG	GTCTTCCAAA	CCTCGACAAG	2880
GCATGGGGAC	GAATCTTTCT	GTTCCCAATC	CTCTGGGATT	CTTTCCCGAT	CACCAGTTGG	2940
ACCTGTCATT	CGGAGCCAAC	TCAAACAATC	CAGATTGGGA	CTTCAACCCC	AACAAGGATC	3000
ATTGGCCAGA	GGCAAATCAG	GTAGGAGCGG	GAGCATTTGG	GCCAGGGTTC	ACTCCACCAC	3060
ACGGCGGTCT	TTTGGGGTGG	AGCCCTCAGG	CTCAGGGCAT	ATTGACAACA	GTGCCAGCAG	3120

CGCCTCCTCC TGCCTCTACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC 3180  
 CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG 3215

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3212 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

AACTCCACCA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTTCCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGCG CCGAACATGG AGAACACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GACTTCTCTC AATTTTCTAG GGGGAGCACC CACGTGTCCT	300
GGCCAAAATT CGCAGTCCCC AACCTCCAAT CACTCACCAA CCTCTTGTC TCCAATTTGT	360
CCTGGCTATC GCTGGATGTG TCTGCGGCGT TTTATCATAT TCCTCTTCAT CCTGCTGCTA	420
TGCCTCATCT TCTTGTTGGC TCTTCTGGAC TACCAAGGTA TGTTGCCCGT TTGTCCTCTA	480
CTTCCAGGAA CATCAACTAC CAGCACGGGA CCATGCAAGA CCTGCACGAT TCCTGCTCAA	540
GGAACCTCTA TGTTTCCCTC TTGTTGCTGT ACAAACCTT CGGACGGAAA TTGCACTTGT	600
ATTCCCATCC CGTCATCTTG GGCTTTCGCA AGATTCTAT GGGAGTGGGC CTCAGTCCGT	660
TTCTCCTGGC TCAGTTTACT AGTGCCATTT GTTCAGTGGT TCGCAGGGCT TTCCCCACT	720
GTTTGGCTTT CAGTTATATG GATGATGTGG TATTGGGGGC CAAGTCTGTA CAACATCTTG	780
AGTCCCTTTA TACCTCTATT ACCAATTTTC TTGTGTCTTT GGGTATACAT TTGAACCCTA	840
ATAAAACCAA ACGTTGGGGC TACTCCCTTA ACTTCATGGG ATATGTAATT GGAAGTTGGG	900
GTACGTTACC ACAGGAACAT ATTGTACAAA AAATCAAGCA ATGTTTTTCG AACTGCCTG	960
TAAATAGACC TATTGATTGG AAAGTATGTC AAAGAATTGT GGGTCTTTTG GGCTTTGCTG	1020
CCCCTTTAC ACAATGTGGT TATCCTGCCT TGATGCCTTT ATATGCATGT ATACAAGCTA	1080
AGCAGGCTTT TACTTTCTCG TCAACTTACA AGGCCTTTCT GTGTAAACAA TATCTGCACC	1140
TTTACCCCGT TGCCCGGCAA CGGTCAGGTC TCTGCCAAGT GTTTGCTGAC GCAACCCCCA	1200
CTGGATGGGG CTTGGCCATA GGCCATCGGC GCATGCGTGG AACCTTTGTG GCTCCTCTGC	1260

CGATCCATAC	TGCGGAACTC	CTAGCAGCTT	GTTTTGCTCG	CAGCCGGTCT	GGAGCGAAAC	1320
TTATCGGGAC	TGACAACTCT	GTTGTCCTCT	CTCGGAAATA	CACCTCCTTC	CCATGGCTGC	1380
TCGGATGTGC	TGCCAACTGG	ATCCTGCGCG	GGACGTCCCT	TGTCTACGTC	CCGTCGGCGC	1440
TGAATCCCGC	GGACGACCCG	TCTCGGGGTC	GTTTGGGCCT	CTACCGTCCC	CTTCTTCATC	1500
TGCCGTTCCG	GCCGACCACG	GGGCGCACCT	CTCTTTACGC	GGTCTCCCCG	TCTGTGCCTT	1560
CTCATCTGCC	GGACCGTGTG	CACTTCGCTT	CACCTCTGCA	CGTCGCATGG	AGACCACCGT	1620
GAACGCCCAT	CAGGTGTTGC	CCAAGGTCTT	ATATAAGAGG	ACTCTTGAC	TTTCAGCAAT	1680
GTCAACGACC	GACCTTGAGG	CATACTTCAA	AGACTGTTTG	TTTAAGGACT	GGGAGGAGTT	1740
GGGGGAGGAA	CTTAGGTTAA	TGATCTTTGT	ACTAGGAGGC	TGTAGGCATA	AATTGGTCTG	1800
TTCACCAGCA	CCATGCAACT	TTTTCACCTC	TGCCTAATCA	TCTCTTGTTT	ATGTCCTACT	1860
GTTCAAGCCT	CCAAGCTGTG	CCTTGGGTGG	CTTTAGGACA	TGGACATTGA	CCCATATAAA	1920
GAATTTGGAG	CTTCTGTGGA	GTTACTCTCT	TTTTTGCCCT	CTGACTTCTT	TCCTTCTATT	1980
CGAGATCTCC	TCGACACCGC	CTCTGCTCTG	TATCGGGAGG	CCCTAGAGTC	TCCGGAGCAT	2040
TGTACACCTC	ACCATACAGC	ACTCAGGCAA	GCTATTCTGT	GTTGGGGTGA	GTTGATGAAC	2100
CTGGCCACCT	GGGTGGGAAG	TAATTTGGAA	GATCCAACAT	CCAGGGAAGC	AGTAGTCAGC	2160
TATGTCAATG	TTAATATGGG	CCTAAAACTC	AGACAACAT	TGTGGTTTCA	CATTTCTCTG	2220
CTTACTTTTG	GAAGAGATAC	TGTTCTTGAG	TATTTGGTGT	CTTTTGAGT	GTGGATTCGC	2280
ACTCCTACCG	CTTACAGACC	ACCAAATGCC	CCTATCTTAT	CAACACTTCC	GGAAACTACT	2340
GTTGTTAGAC	GACGAGGCAG	GTCCCCTAGA	AGAAGAACTC	CCTCGCCTCG	CAGACGAAGG	2400
TCTCAATCGC	CGCGTCGCAG	AAGATCTCAA	TCTCGGGAAC	CTCAATGTTA	ATGTCCCTTG	2460
GACTCATAAG	GTGGGAAACT	TTACAGGACT	TTACTCTTCT	ACTGTACCTG	TCTTTAATCC	2520
TGAGTGGCAA	ACTCCCTCCT	TTCCCTAACAT	TCATTTACAG	GAGGACATTA	TTGATAGATG	2580
TCAACAATAT	GTGGGCCCTC	TTACAGTTAA	TGAAAAAAGG	AGATTAAAAT	TAATTATGCC	2640
TGCTAGGTTT	TATCCAAACC	TTACCAAATA	TTTGCCCTTG	GATAAAGGCA	TTAAACCTTA	2700
TTATCCTGAA	CATGCAGTTA	ATCATTACTT	TCAAACCTAGG	CATTATTTAC	ATACTCTGTG	2760
GAAGGCTGGC	ATTCTATATA	AGAGAGAAAC	TACCCGCAGC	GCTTCATTTT	GTGGGTCACC	2820
ATATTCTTGG	GAACAAGAGC	TACAGCATGG	GAGGTTGGTC	TTCCAAACCT	CGACAAGGCA	2880
TGGGGACGAA	TCTTTCTGTT	CCCAATCCCT	TGGGATTCTT	TCCCATCAC	CAGTTGGACC	2940
CTGCGTTCGG	AGCCAACTCA	AACAATCCAG	ATTGGGACTT	CAACCCCAAC	AAGGATCATT	3000
GGCCAGAGGC	CAATCAGGTA	GGAGTGGGAG	CATTCGGGCC	AGGGTTCACC	CCACCACACG	3060
GCGGTCTTTT	GGGGTGGAGC	CCTCAGGCTC	AGGGCATATT	GACAACAGTG	CCAGCAGCGC	3120
CTCCTCCTGC	CTCTACCAAT	CGGCAGTCAG	GAAGACAGCC	AACTCCCATC	TCTCCACCTC	3180
TAAGAGACAG	TCATCCTCAG	GCCATGCAGT	GG			3212

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3215 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299;

AACTCCACAA CATTCCAACA AGCTCTGCAG GATCCCAGAG TCAGGGTCCT TTATTTTCCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC TCTCATTTTCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGTA ACGAACATGG AGAACACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCGTGTGT	300
CCTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTC	480
CTACTTCCAG GAACATCAAC TACCAGCAGG GGACCATGCA AGACCTGCAC GATTCTGCT	540
CAAGGAACCT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTTGGACGG AACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GTAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGCGCCA TTTGTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTTAAACC	840
CTAATAAAAC CAAAAGATGG GGCTATTCCC TTAACCTCAT GGGCTATGTA ATTGGAAGTT	900
GGGGTACCTT ACCACAAGAA CATATTGTAC TAAAAATCAC ACAATGTTTT CGAAAACCTC	960
CTGTTAATAG GCCTATTGAT TGGAAAGTGT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCCTT TACACAATGT GGGTATCCTG CCTTAATGCC CTTGTATGCC TGTATTCAAG	1080
CTAAGCAGGC TTTCACCTTC TCGCCAACTT ATAAGGCCTT TCTGTGTAAA CAATATCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCTG GTCTTTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATGGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCGG CTTGTTTTGC TCGCAGCCGG TCTGGAGCAA	1320
ACATTATCGG AACCGACAAC TCTGTCTGCC TCTCTCGGAA ATACACATCC TTTCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTAC GCGGGACGTC CTTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGCG GCCGTTTGGG GCTCTACCGT CCCCTTCTTT	1500



GTCTGCGGTT CCGGCCAACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAAACCAC	1620
CGTGAACGCC CACATGGTCT TGCCCAAGGT CTTGCATAAG AGAACTCTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATATTT CAAAGACTGT GTGTTCAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGGTTAGAT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTTCTGT GGAGTTACTC TCTTTTTTGC CTTCTGATTT CTTTCCATCT	1980
ATTCGAGACC TCCTCGACAC CGCCTCAGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAG	2040
CATTGTTTAC CTCACCATAC AGCACTCAGG CAAGCTGTTT TGTGTTGGGG TGAGTTAATG	2100
AATCTGGCTA CCTGGGTGGG AAGTAATTTG GAAGACCCAG CATCAAGAGA ATTGGTAGTC	2160
AGTTATGTCA ATGTTAATAT GGGCCTAAAA ATCAGGCAAC TGTGTGGTT TCATATTTCC	2220
TGTCTTACTT TTGGAAGAGA AACTGTCTT GAGTACTTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CGCCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGAAGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCCCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTTAA	2520
TCCTGAATGG CAAACTCCCT CTTTTCTGA CATTCAATTTG CAGGAGGACA TTATTAATAG	2580
ATGTCAACAA TATGTGGGCC CTCTTACAGT TAATGAAAAA AGAAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTTTATCCTA ACCTTACTAA ATATTTGCC TTAGACAAAG GCATTAAACC	2700
TTATTATCCA GAACAGACAG TTAATCATT CTTCAAACT AGGCATTATT TGCATACTCT	2760
GTGGAAGGCT GGTAGTCTAT ATAAGAGAGA AACTACACGC AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGAACAAG AGCTACAGCA TGGGAGGTTG GTCTTCAAAA CCTCGGAAAG	2880
GCATGGGGAC GAATCTTTCG GTACCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940
ACCCTGCGTT CGGAGCCAAC TCAAACAATC CCGATTGGGA CTTCAACCCC AACAAGGATC	3000
ACTGGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTCGG GCCAGGGTTC ACCCCACCAC	3060
ACGGAGGTCT TTTGGGGTGG AGCCCTCAGG CCCAGGGCAT ATTGACAACA GTGCCAGCAG	3120
CTCCTCCTTC TGCCTCCACC AATCGGCAGT CAGGAAGACA GCCTACGCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

AACTCCACAA CATTCCAACA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTAAAC CCTGTTCGA CTAAGCCTC TCTCATTTCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGTA ACGAACATGG AGAACACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGGG GTGGACTTCT CTCAATTTTC TAGGGGAAGC ACCAAGGTGT	300
CCTGGCCAAA ATTGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TCTTCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCCTGCT	540
CAAGGAACCT CTATGTTTCC CTCATGTTGC TGTACAAAAC CTTCCGACGG AAAGTGCCT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GTAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGCGCCA TTTGTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATACCTCT ATTACCAATT TTCTTTTGT TTTGGGTATA CATTGAACC	840
CTAATAAGAC CAAAAGATGG GGCTATTCCC TTAACCTCAT GGGCTATGTA ATTGGAAGTT	900
GGGTACCTT ACCACAAGAA CATATTGTAC TAAAAATCAA ACAATGTTTT CGAAAACCTC	960
CTGTAAATAG GCCTATTGAT TGGAAGGTCT GCCAAAGAAT TGTGGGTCTT TTGGGATTTG	1020
CTGCCCCTTT TACACAATGT GGATATCCTG CCTTAATGCC TTTGTATGCA TGTATTCAAG	1080
CTAAGCAAGC TTTCACTTTT TCGTCAACTT ACAAAGCCTT TCTGTGTAAC CAATATCTGA	1140
ACCTTTACCC CGTTGCCCCG CAACGGTCTG GTCTCTGCCA AGTGTCTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATTGGCAATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AACTTATCGG AACTGACAAC TCTGTCTGCC TCTCTCGCAA ATACACATCC TTTCCATGGC	1380
TGCTCGGCTG TGCTGCCAAC TGGATCCTAC GAGGGACGTC CTTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTTGGG GATCTACCGT CCCCTTCTTC	1500
GTCTGCGGTT CCGGCCAACC ACGGGGCGCA CCTCTCTTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTCACTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACATGGTAT TGCCCAAGGT CTTGCATAAG AGGACTCTTG GACTCTCAGC	1680

GATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT GTATTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGAT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTTCTGT GGAGTTACTC TCTTTTTTGC CTTCTGATTT CTTTCCATCT	1980
ATTCGAGACC TCCTCGACAC CGCCTCAGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTTAC CTCACCATAC AGCACTCAGG CAAGCTGTTT TGTGTTGGGG TGAGTTAATG	2100
AATCTGGCTA CCTGGGTGGG AAGTAATTTG GAAGACCCAG CATCCAGGGA ATTAGTGGTC	2160
AGTTATGTCA ACATTAATAT GGGCCTAAAA ATCAGACAAC TATTGTGGTT TCACATTTC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAGTATTTGG TGTCTTTTGG AGTGTGGATT	2280
CGCACTCCTC CCGCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGTCGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CACCGCGTCG CAGAAGATCT CAATCTCGGG AATCCCAATG TTAGTATCCC	2460
TTGGAATCAT AAGGTGGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTTAA	2520
TCCTGAATGG CAAACTCCCT CTTTTCCTGA CATTCAATTTG CAGGAGGACA TTATTAATAG	2580
ATGTCAACAA TATGTGGGCC CTCTTACAGT TAATGAAAAA AGAAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTTTATCCTA ACCTTACCAA ATATTTGCCC TTAGATAAAG GCATTAAACC	2700
TTATTATCCT GAACATGCAG TTAATCATTA CTTCAAAACA AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATCTTAT ATAAAAGAGA AACTACACGC AGTGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTG GTCTTCCAAA CCTCGGAAAG	2880
GCATGGGGAC GAATCTTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940
ACCCTGCATT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAGGATC	3000
AATGGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTGCG GCCAGGGTTC ACCCCACCAC	3060
ACGGAGGTCT TTTGGGGTGG AGCCCTCAGG CACAAGGCAT ATTGACAACA CTGCCAGCAG	3120
CTCCTCCTCC TGCTCCACC AATCGGCAGT CAGGAAGACA GCCTACGCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

AATCCACAA CTTCCACCA AACTCTACAA GATCCCCCTG CTGGTGGCTC CAGTTCAGGA	60
ACAGTAAACC CTGTTCCGAC TACTGTCTCT CACATATCGT CAATCTTCAC GAGGATTGGG	120
GACCCTGCAC TGAACATGGA GAACATCACA TCAGGATTCC TAGGACCCCT GCTCGTGTTA	180
CAGGCGGGGT TTTTCTTGTT GACAAGAATC CTCACAATAC CGCAGAGTCT AGACTCGTGG	240
TGGACTTCTC TCAATTTTCT AGGGGGAACCT ACCGTGTGTC TTGGCCAAAA TTCGCAGTCC	300
CCAACTCCA ATCACTCACC AACCTCCTGT CCTCCAACCTT GTCCTGGTTA TCGCTGGATG	360
TGTCTGCGGC GTTTTATCAT CTTCCTCTTC ATCCTGCTGC TATGCCTCAT CTTCTTGTTG	420
GTTCTTCTGG ACTATCAAGG TATGTTGCCC GTTTGTCCTC TAATCCAGG ATCTTCAACC	480
ACCAGCACGG GACCATGCAG GACCTGCAG ACTCCTGCTC AAGGCAACTC TATGTATCCC	540
TCCTGTTGCT GTACCAAACC TTCGGACGGA AATTGCACCT GTATTCCCAT CCCATCATCT	600
TGGGCTTTCTG GAAAATTCCT ATGGGAGTGG GCCTCAGCCC GTTCTCCTG GCTCAGTTTA	660
CTAGTGCCAT TTGTTCAAGT GTTCGTAGGG CTTTCCCCCA CTGTTTGGCT TTCAGTTATA	720
TGGATGATGT GGTATTGGGG GCCAAGTCTG TACAGCATCT TGAGTCCCTT TTTACCGCTG	780
TTACCAATTT TCTTTTGTCT TTGGGCATAC ATTTAAACCC TAACAAAACA AAAAGATGGG	840
GTTACTCTTT ACACTTCATG GGCTATGTCA TTGGATGTTA TGGGTCATTG CCACAAGATC	900
ACATCAGACA GAAAATCAAA GAATGTTTGA GAAAACCTCC TGTTAACAGG CCTATTGATT	960
GGAAAGGCTG TCAACGAATT GTGGGTTTAT TGGGTTTTGC TGCCCCTTTT ACACAATGTG	1020
GTTATCCTGC GTTGATGCCT TTGTATGCAT GTATTCAATC TAAGCAGGCT TTCACTTTCT	1080
CGCCAACTTA CAAGGCCTTT CTGTGTAAAC AATACCTGAA CCTTTACCCC GTTGCCCGGC	1140
AACGGCCAGG TCTGTGCCAA GTGTTTGCTG ACGCAACCCC CACTGGCTGG GGCTTGGTCA	1200
TGGGCCATCA GCGCATGCGT GGAACCTTTC GGGCTCCTCT GCCGATCCAT ACTGCGGAAC	1260
TCCTAGCCGC TTGTTTTGCT CGCAGCAGGT CTGGAGCAAA CATTCTCGGG ACGGATAACT	1320
TTGTTGTCTT ATCCCGCAAA TATACATCGT TTCCATGGCT GCTAGGCTGT GCTGCCAACT	1380
GGATCCTGAG CGGGACGTCC TTCGTTACG TCCCGTCGGC GCTGAATCCA GCGGACGACC	1440
CTTCTCGGGG CCGCTTGGGA CTCTCTCGTC CCCTTCTCCG TCTGCCGTTT CGTCCGACCA	1500
CGGGGCGCAC CTCTCTTTAC GCGGACTCCC CGTCTGTGCC TTCTCATCTG CCGGACCGTG	1560
TGCACTTCGC TTCACCTCTG CACGTCGCAT GGAGACCACC GTGAACGCCC ACCAATTCTT	1620
GCCCAAGGTC TTACATAAGA GGAATCTTGG ACTCTCAGCA ATGTCAACGA CCGACCTTGA	1680
GGCATACTTC AAAGACTGTT TGTTTAAAGA GTGGGAGGAG TTGGGGGAGG AGATTAGATT	1740
AAAGTTGTTT GTATTAGGAG GCTGTAGGCA TAAATTGGTC TGCGCACCAG CACCATGCAA	1800
CTTTTTCACC TCTGCCTAAT CATCTCTTGT TCATGTCCTA CTGTTCAAGC CTCCAAGCTG	1860

TGCCTTGGGT GGCTTTAGGA CATGGACATT GATCCTTATA AAGAATTGG AGCTTCTATG	1920
GAGTTGCTCT CGTTTTTGCC TTCTGACTTC TATCCTTCAG TACGAGATCT TCTAGATACC	1980
GCCTCAGCTC TATATCGGGA AGCCTTAGAG TCTCCTGAGC ATTGTACACC TCATCATACT	2040
GCACTCAGGC AAGCAATTCT TTGCTGGGGG GAATTAATGA CTCTAGCCAC CTGGGTGGGT	2100
GGTAATTTGC AAGATCCAAC ATCCAGGGAC CTAGTAGTCA GTTATGTAA CACTAATATG	2160
GGCCTAAAGT TCAGGCAACT ATTGTGGTTT CACGTTTCTT GTCTCACTTT TGGAAGAGAA	2220
ACAGTCGTAG AGTATTTGGT GTCTTTTGGA GTGTGGATTC GCACTCCTCA AGCTTATAGA	2280
CCACCAAATG CCCCTATCTT ATCAACACTT CCGGAGACTT GTGTTGTTAG ACGACGAGGC	2340
AGGTCCCCTA GAAGAAGAAC TCCCTCGCCT CGCAGACGAA GGTCTCAATC GCCGCGTCGC	2400
AGAAGATCTC AATCTCGGGA ATCTCAATGT TAGTATTCCT TGGACTCATA AGGTGGGAAA	2460
CTTTACGGGG CTTTATTCTT CTA CTGTTCC TGTCTTTAAC CCTCATTGGA AAACACCCTC	2520
TTTTCTAAT ATACATTTAC ACCAAGACAT TATCAAAAAA TGTGAACAAT TTGTAGGCCC	2580
ACTCACAGTC AATGAGAAAA GAAGACTGCA ATTGATTATG CCTGTCAGGT TTTATCCAAT	2640
GGTTACCAA TATTTGCCAT TGGATAAGGG TATTAAACCG TATTATCCAG AACATCTAGT	2700
TAATCATTAC TTCCAAACCA GACATTATTT ACACACTCTA TGAAGGCCG GTGTATTATA	2760
TAAGAGAGAA ACAACACATA GCGCCTCATT TTGTGGATCA CCATATTCTT GGGAACAAGA	2820
GATACAGCAT GGGGCAGAAT CTTTCCACCA GCAATCCTCT GGGATTCTTT CCCGACCACC	2880
AGTTGGATCC AGCCTTCAGA GCAAACACCG CAAATCCAGA TTGGGACTTC AATCCCAACA	2940
AGGACACCTG GCCAGACGCC AACAAGGTAG GAGCTGGAGC ATTCTGGGCTG GGAATCACC	3000
CACCGCACGG AGGCCTTTTG GGGTGGAGCC CTCAGGCTCA GGGCATACTA CAGACCGTGC	3060
CAGCAAATCC GCCTCCTGCC TCTACCAATC GCCAGACAGG AAGGCAGCCT ACCCCTCTGT	3120
CTCCACCTTT GAGAGACACT CATCCTCAGG CCATGCAGTG G	3161

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AACTCCACAA CCTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT GTATTTCCCT

GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCCGA CTA CTGCTC TCACCTATCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGCG CTGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TTCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC TACCGTGTGT	300
CTTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAAC	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GATCCTCAAC CACCAGCACG GGACCATGCC GAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTATCC CTCCTGTTGC TGTACCAAAC CTTCGGACGG AAATTGCACC	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTTCACTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGCATC	780
TTGAGTCCCT TTTTACCGCT GTTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAGAGATGG GGTACTCTC TAAATTTTAT GGGCTATGTC ATTGGATGTT	900
ATGGGTCCCTT GCCACAAGAA CACATCATAC AAAAAATCAA AGAATGTTTT AGAAAACCTC	960
CTGTTAACAG GCCTATTGAT TGGAAAGTAT GTCAACGAAT TGTGGGTCTT TTGGGTTTTG	1020
CTGCCCCCTT TACTCAATGT GGTATCCTG CTTTAATGCC CTGTATGCA TGTATTCAAT	1080
CTAAGCAGGC TTTCACTTC TCGCCAACTT ACAAGGCCCTT TCTGTGTAAC CAATACCTGA	1140
ACCTTTACCC CGTTGCCGGG CAACGGCCAG GTCTATGCCA AGTGTCTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGCT ATGGGCCATC AGCGCATGCG TGGAACTTT TCGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCAGG TCTGGAGCAA	1320
ACATTATCGG GACTGATAAC TCTGTTGTCC TCTCCCGCAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GTCGCTTGGG ACTCTCTCGT CCCCTTCTCC	1500
GTCTGCCGTT CCGACCGACC ACGGGGCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCTGACCTT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCAAATAT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCTGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGAT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCTTG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTACCGT GGAGTTACTC TCGTTTTTGC CTTCTGACTT CTTTCCTTCA	1980
GTACGAGATC TTCTAGATAC CGCCTCAGCT CTGTATCGGG ATGCCTTAGA GTCTCCTGAG	2040
CATTGTTTAC CTCACCATAC TGCACTCAGG CAAGCAATTC TTTGCTGGGG GGAACCTAATG	2100

ACTCTAGCTA CCTGGGTGGG TGTTAATTTG GAAGATCCAG CATCTAGGGA CCTAGTAGTC	2160
AGTTATGTCA ACACATAATAT GGGCCTAAAG TTCAGACAAC TCTTGTGGTT TCACATTTCT	2220
TGTCTCATTT TTGGAAGAGA AACAGTTATA GAGTATTTGG TGTCTTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCC TATCAACACT TCCGGAGACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGGA ATTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTTAA	2520
TCCTCATTGG AAAACACCAT CTTTTCCTAA TATACATTTA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAG TTTGTAGGCC CACTCACAGT TAATGAGAAA AGAAGATTGC AATTGATCAT	2640
GCCTGCTAGG TTTTATCCAA AGGTTACCAA ATATTTACCA TTGGATAAGG GTATTAAACC	2700
TTATTATCCA GAACATCTAG TTAATCATT A CTTCAAACT AGACACTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGAGA AACAACACAT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG ATCTACAGCA TGGGGCAGAA TCTTTCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTCGGGCT GGGTTTCACC CCACCGCAG GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACAAACCTTG CCAGCAAATC CGCCTCCTGC CTCCACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCTCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

AACTCCACAA CTTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT ATATTTCCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC TCCCTTATCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGTG ACGAATATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC GAGGGGGAAC TACCGTGTGT	300

CTTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAACT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG GGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GAGTATCAAG GTATGTTGCA CGTTTGTCTT	480
CTAATTCCAG GAACAACAAC AACCAGTACG GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGCAACT CTATGTTTCC CTCATGTTGC TGTACCAAAA CTTCGGATGG AAATTGCACC	600
TGTATTCCCA TCCCATCGTC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCAGT GGTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTTACGCTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGCATC	780
TTGAGTCCCT TTTTACCGCT GTTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAGAGATGG GGTACTCTT TACATTTTAT GGGCTATGTC ATTGGATGTT	900
ATGGGTCTTT GCCACAAGAA CACATCATAC AAAAAATCAA AGAATGTTTT AGAAAAGTTC	960
CTGTTAACAG GCCTATTGAT TGGAAAAGTAT GTCAACGAAT TGTGGGTCTT TTAGGTTTTG	1020
CTGCCCCCTT CACACAATGT GGTATCCTG CTTTAATGCC CTTGTATGCT TGTATTCAAT	1080
TTAAGCAGGC TTTCACTTTC TCGCCAACTT ACAAGGCCCTT TCTGTGTAAA CAATACCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGCCAG GTCTATGCCA AGTGTGCTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGGT ATGGGCCATC AGCGCATGCG TGGAACTTTT TCGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CCTGTTTTGC TCGCAGCAGG TCTGGAGCAA	1320
ACATTCTCGG GACGGATAAC TCTGTGTTT TCTCCCGCAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTGTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCTTCTCGGG GCCGCTGGG ACTCTCTCGT CCCCTTCTCT	1500
GTCTGCCGTT TCGACCGACC ACGGGGCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CATCAGATCC TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCCCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTTAAGG ACTGGGAGGA	1740
GCTGGGGGAG GAGATTAGGT TAAAGGTCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCTTG TACATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTACTGT GGAGTACTC TCGTTTTTGC CTTCTGACTT CTTTCCTTCC	1980
GTACGAGATC TCCTAGACAC CGCCTCAGCT CTGTATCGGG AAGCCTTAGA GTCTCCTGAG	2040
CATTGTTTAC CTCACCATAC TGCACTCAGG CAAGCAATTC TTTGCTGGGG GGAACATAATG	2100
ACTCTAGCTA CCTGGGTGGG TGTTAATTTG GAAGATCCAG CATCTAGAGA CCTAGTAGTC	2160
AGTTATGTCA AACTAATAT GGGCTTAAAG TTCAGGCAAC TCTGTGGTT TCACATTTCT	2220
TGTCTCACTT TTGGAAGAGA AACAGTTATA GAGTATTGG TGGCTTTCGG AGTGTGGATT	2280



CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCC TATCAACACT TCCGGAGACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACGGG GTTTTATTCT TCTACTGTTT CTGTCTTTAA	2520
CCCTCATTGG GAAACCCCCT CTTTTCCTAA TATACATTTA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAG TTTGTAGGCC CACTCACAGT TAATGAGAAA AGAAGATTGC AATTGATTAT	2640
GCCTGCTAGG TTTTATCCAA AGGTTACCAA ATATTTACCA TTGGATAAGG GTATTAAACC	2700
TTATTATCCA GAACATCTAG TTAATCATT CTTCCAAACT AGACACTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGAGA AACAACACAT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG ATCTACAGCA TGGGGCAGAA TCTATCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTCCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGAT GGAGCTGGAG	3000
CATTCCGGCT GGGACTCACC CCACCGCAGG GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACACACCGTG CCAGCAAATC CGCCTCCTGC CTCTACCAAT CGCCAGACAG	3120
GAAGGCAACC TACCCCTCTG TCTCCACCTT TGAGAGACAC TCATCCTCAG GCCGTGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AACTCCACAA CCTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT GTATTTCCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCTGA CTACTGCCTC TCCCTTATCG	120
TCAATCTCCG CGAGGACTGG GGACCCTGCA CTGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC TACCGTGTGT	300
CTTGGCCAAA ATTGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAACT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TCTTCCTCTT CATCCTGCTG	420

CTATGCCTCA	TCTTCTTGTT	GGTTCTTCTG	GACTATCAAG	GTATGTTGCC	CGTTTGTCTT	480
CTAATTCCAG	GATCTTCAAC	AACCAGCAG	GGACCATGCA	GAACCTGCAC	GACTCCTGCT	540
CAAGGAACCT	CTATGTATCC	CTCCTGTTGC	TGTACCAAAC	CTTCGGACGG	AAATTGCACC	600
TGTATTCCCA	TCCCATCATC	TTGGGCTTTC	GGAAAATTCC	TATGGGAGTG	GGCCTCAGCC	660
CGTTTCTCCT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTCAGT	GGTTCGTAGG	GCTTTCCCCC	720
ACTGTTTGGC	TTTCAGTTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAGCATC	780
TTGAGTCCCT	TTTTACCGCT	GTTACCAATT	TTCTTTTGTC	TCTGGGTATA	CATTTAACCC	840
CTAACAAAAC	AAAAAGATGG	GGTATTCCC	TAAACTTCAT	GGGTACATA	ATTGGAAGTT	900
GGGGAACGTT	GCCACAAGAT	CATATTGTAC	AAAAGATCAA	AGAATGTTTT	AGAAAACCTC	960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTAT	GGCAACGAAT	TGTGGGTCTT	TTGGGCTTTC	1020
CTGCTCCATT	TACACAATGT	GGATATCCTG	CCTTAATGCC	TTTGTATGCC	TGTATACAAG	1080
CTAACACAGG	TTTCACTTTC	TCGCCAAGTT	ACAAGGCCTT	TCTAAGTAAA	CAGTACATGA	1140
ACCTTTACCC	CGTTGCTCGG	CAACGGCCTG	GTCTGTGCCA	AGTGTTCGCT	GACGCAACCC	1200
CCACTGGCTG	GGGCTTGGCA	ATAGGCAATC	AGCGCATGCG	TGGAACCATT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTTTTGC	TCGCAGCCGG	TCTGGGGCAA	1320
AGCTCATCGG	AACTGACAAT	TCTGTTGTCC	TCTCGCGGAA	ATATACATCG	TTCCATGGC	1380
TGCTAGGTTG	TACTGCCAAC	TGGATCCTTC	GCGGGACGTC	CTTTGTTTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCTTCTCGGG	GCCGCTTGGG	ACTCTCTCGT	CCCCTTCTCC	1500
GTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGTCCGT	GTGCACTTCG	CTTCACCTCT	GCACATTGCA	TGGAGACCAC	1620
CGTGAACGCC	CATCAGATTA	TGCCCCAAGG	TTTACATAAG	AGGACTCTTG	GACTCCCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCCTACTT	CAAAGACTGT	GTGTTTAAGG	ACTGGGAGGA	1740
GCTGGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTATTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTTCAC	CTCTGCCTAA	TCATCTCTTG	TTCATGTCTT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTAGG	GCATGGACAT	TGACCCCTAT	1920
AAACAATTTG	GAGCTACTGT	GGAGTTACTC	CCGTATTTGC	CTTCTGACTT	CTTTCTCTAC	1980
GTACGAGATC	TCCTAGATAC	CGCCTCAGCT	CTGTATCGGG	AAGCCTTAGA	GTCTCCTGAG	2040
CATTGTTTAC	CTCACCATAC	TGCACTCAGG	CAAGCAATTC	TTTGCTGGGG	GGAACATAATG	2100
ACTCTAGCTA	CCTGGGTGGG	TGTTAATTTG	GAAGATCCAG	CATCTAGAGA	CTTAGTAGTC	2160
AGTTATGTCA	ACACTAATAT	GGGCCTAAAG	TTCAGGCAAC	TCTTGTGGTT	TCACATTCTT	2220
TGTCTCACTT	TTGGAAGAGA	AACAGTTATA	GAGTATTTGG	TGTCTTTCGG	AGTGTGGATT	2280
CGCACTCCTC	CAGCTTATAG	ACCACCAAAT	GCCCCATATC	TATCAAACT	TCCGGAGACT	2340
ACTGTTGTTA	CACGACGAGG	CAGGTCCCCCT	AGAAGAAGAA	CTCCCTCGCC	TGCCAGACCA	2400

AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGGA ACTTTACGGG GCTTTATTCT TCTACTGTTC CTGTCTTTAA	2520
TCCTCATTGG AAAACACCTT CTTTTCCTAA TATACATTTA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAA TTTGTAGGCC CACTCACAGT CAATGAGAAA AGAAGACTGC AATTGATTAT	2640
GCCTGCTAGG TTTTATCCAA ATGTCACCAA ATATTTGCCA TTGGATAAGG GTATTAAACC	2700
TTATTATCCA GAGCATCTAG TTAATCATT CTTCCAAACC AGACATTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGAGA AACAAACAT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGGCAGAA TCTTTCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTGGGGCT GGGTTTCACC CCACCGCAGC GAGGTCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACATACCGTG CCAGCAAATC CGCCTCCTGC CTCTACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCTCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

AACTCCACAA CCTTCCACCA AACTCTGCAA GATCCAAGAG TGAGAGGCCT GTATTTCCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCTGA CTACTGCCTC TCCCTTATCG	120
TCAATCTCCG CGAGGACTGG GGACCCTGTG ACGATCATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT AGAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC TACCGTGTGT	300
CTTGGCCAAA ATTCGCAGTC CCCAACCTCC CATCACTCAC CAACCTCCTG TCCTCCAATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GTACTTCAAC AACCAGCAGC GGACCATGCA GAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTATCC CTCCTGTTGC TGTACCAAAC CTTGGGACGG AAATGCACC	600

TGTATTCCCA	TCCCATCATC	TTGGGCTTTC	GGAAAATTCC	TATGGCAGTG	GGCCTCAGCC	660
CGTTTCTCCT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTCAGT	GGTTCGTAGG	GCTTTCCCCC	720
ACTGTTTGGG	TTTCAGCTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAGCATC	780
GTGAGTCCCT	TTATACCGCT	GTTACCAATT	TTCTTTTGTC	TCTGGGTATA	CATTTAAACC	840
CTAACAAAAC	AAAAAGATGG	GGTTATTCCC	TAAACTTCAT	GGGTACATA	ATTGGAAGTT	900
GGGGAACGTT	GCCACAGGAT	CATATTGTAC	AAAAGATCAA	ACACTGTTTT	AGAAAACTTC	960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTAT	GGCAACGAAT	TGTGGGTCTT	TTGGGTTTTG	1020
CTGCTCCATT	TACACAATGT	GGTTATCCTG	CCTTAATGCC	TTTGTATGCC	TGTATACAAG	1080
CTAAACAGGC	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTAAGTAAA	CAGTACATGA	1140
ACCTTTACCC	CGTTGCTCGG	CAACGGCCTG	GTCTGTGCCA	AGTGTTCGCT	GACGCAACCC	1200
CCACTGGCTG	GGGCTTGCCA	TAGGGCCATC	AGCGCATGCG	TGGAACCTTT	GAGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTTTTGC	TCGCAGCAGG	TCTGGAGCAA	1320
ACATTATCGG	GACTGATAAC	TCTGTTGTCC	TATCGCGGAA	ATATACATCG	TTTCCATGGC	1380
TGCTAGGTTG	TACTGCCAAC	TGGATCCTTC	GCGGGACGTC	CTTTGTTTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCCTCTCGGG	GCCGCTTGGG	ACTCTCTCGT	CCCCTTCTCC	1500
GTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGTCTCA	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGTCCGT	GTGCACTTCG	CTTCACCTCT	GCACGTGCA	TGGAGACCAC	1620
CGTGAACGCC	CATCAAAGTC	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCCCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCCTACTT	CAAAGACTGT	GTGTTTAAGG	ACTGGGAGGA	1740
GCTGGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTATTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTTTAC	CTCTGCCTAA	TCATCTCTTG	TTCATGTCCC	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTGGG	GCATGGACAT	TGACCCTTAT	1920
AAAGAATTTG	GAGCTACTGT	GGAGTTACTC	TCGTTTTTGC	CTTCTGACTT	CTTTCCTTCC	1980
GTAAGAGATC	TCCTAGACAC	CGCCTCAGCT	CTGTATCGAG	AAGCCTTAGA	GTCTCCTGAG	2040
CATTGCTCAC	CTCACCATAC	TGCACTCAGG	CAAGCCATTC	TCTGCTGGGG	GGAAGTGATG	2100
ACTCTAGCAT	CCTGGGTGGG	TGATAAATTTG	GAAGATCCAG	CGTCTAGGGA	CCTAGTAGTC	2160
AGTTATGTTA	ACACTAATAT	GGGCCTAAAG	ATCAGGCAAC	TATTGTGGTT	TCATATATCT	2220
TGCCTTACTT	TTGGAAGAGA	GACTGTACTT	GAATATTTGG	TCTCTTTCGG	AGTGTGGATT	2280
CGCACTCCTC	CAGCCTATAG	ACCACCAAAT	GCCCCATCT	TATCAAACT	TCCGGAACT	2340
ACTGTTGTTA	GACGACGGGA	CAGGTCCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGGTCTCAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCGGG	AATCTCAATG	TTAGTATTCC	2460
TTGGACTCAT	AAGGTGGGGA	ACTTTACTGG	GCTTTATTCT	TCTACTGTAC	CTGTCTTTAA	2520
TCCTCATTGG	AAAACACCAT	CTTTTCCTAA	TATACATTTA	CACCAAGACA	TTATCAAAAA	2580

ATGTGAACAG TTTGTAGGCC CACTCACAGT TAATGAGAAA AGAAGATTGC AATTGATTAT	2640
GCCTGCTAGG TTTTATCCAA AGGTTACCAA ATATTTACCA TTGGATAAGG GTATTAAACC	2700
TTATTATCCA GAACATCTAG TTAATCATT CTTCCAAACT AGACACTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGAGA AACAAACAT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG ATCTACAGCA TGGGGCAGAA TCTATCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTCGGGCT GGGTTTCACC CCACCGCACG GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACAAACCTTG CCAGCAAATC CGCCTCCTGC CTCCACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCTCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AACTCCACAA CCTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT GTATCTCCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCCGA CTACTGTCTC TCCCATATCG	120
TCAATCTTCT CGAGGATTGG GGACCTGCG CTGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCGAAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC CACCGTGTGT	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAACT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTGATTCCAG GATCTTCAAC CACCAGCACG GGACCATGCA GAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTATCC CTCCTGTTGC TGTACCAAAC CTTCGGACGG AAATTGCACC	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTCGTAGG GCTTTCCCCC	720

ACTGTTTGGC	TTTtagttat	ATGGATGATG	TGGTATTGGG	GGCCAAAAC	G TTCACCATC	780
TTGAGTCCCT	TTTTACCGCT	GTTACCAATT	TTCTTTTGTC	TTTGGGTATA	CATCTAAACC	840
CTAACAAAAC	AAAAAGATGG	GGTTACTCTT	TACATTTTAT	GGGCTATGTC	ATTGGATGTT	900
ATGGGTCTTT	GCCACAAGAT	CACATCATAC	AGAAAATCAA	AGAATGTTTT	AGAAAAC TTC	960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTCT	GTCAACGTAT	TGTGGGTCTT	TTGGGATTTG	1020
CTGCTCCTTT	TACACAATGT	GGTTATCCTG	CTTTAATGCC	CTTGTATGCA	TGTATTCAAT	1080
CTAAGCAGGC	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTGTGTAAA	CAATACCTGA	1140
ACCTTTACCC	CGTTGCCCGG	CAACGCCCAG	GTCTGTGCCA	AGTGT TTGCT	GACGCAACCC	1200
CCACTGGCTG	GGGCTTGGTC	ATGGGCCATC	AGCGCATGCG	TGGAACCTTT	CAGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTTTTGC	TCGCAGCCGG	TCTGGAGCAA	1320
ACATTCTCGG	GACGGATAAC	TCTGTTGTTC	TCTCCCGCAA	ATATACGTCG	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTTGTTTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCTTCTCGGG	GCCGCTTGGG	ACTCTCTCGT	CCCCTTCTCC	1500
GTCTGCCGTT	TCGACCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGACTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CACCAATTCT	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCTCTGT	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	TTGTTTAAGG	ACTGGGAGGA	1740
GTGGGGGAG	GAGATTAGAT	TAATGATCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTTTAC	CTCTGCCTAA	TCATCTCTTG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTAGG	ACATGGACAT	TGATCCTTAT	1920
AAAGAATTTG	GAGCTACTGT	GGAGTTACTC	TCGTTTCTGC	CTTCTGACTT	CTTTCCTTCA	1980
GTACGAGATC	TTCTAGATAC	CGCCTCAGCT	CTATATCGGG	AAGCCTTAGA	ATCTCCTGAG	2040
CATTGTTTAC	CTCACCATAC	TGCACTCAGG	CAAGCAATTC	TCTGCTGGGG	GGATCTAATA	2100
ACTCTATCCA	CCTGGGTGGG	TGGTAATTTG	GAAGATCCAA	CATCTAGGGA	CCTAGTAGTC	2160
AGTTATGTTA	ACACTAATAT	GGGCCTAAAG	TTCAGGCAAC	TATTGTGGTT	TCACATTTCT	2220
TGTCTCACTT	TTGGAAGAGA	AACGGTCATA	GAGTATTTGG	TGTCTTTTGG	AGTGTGGATT	2280
CGCACTCCTC	CAGCTTATAG	ACCACCAAAT	GCCCCATCT	TATCAACACT	TCCGGAGACT	2340
ACTGTTGTTA	GACGACGAGG	CAGGTCCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGGTCTCAAT	CGCCACGTCG	CAGAAGAACT	CAATCTCGGG	AATCTCAATG	TTAGTATTCC	2460
CTGGACTCAT	AAGGTGGGAA	ACTTTACGGG	GCTTTATTCT	TCTACTGTTC	CTGTCTTTAA	2520
CCCTCATTTG	AAAACACCCCT	CTTTTCCTAA	TATACATTTA	CACCAAGACA	TTATCAAAAA	2580
ATGTGAACAA	TTTGTAGGCC	CACTCACAGT	CAATGAGAAA	AGAAGACTGC	AATTGATTAT	2640
GCCTGCTAGG	TTTTATCCAA	AGGTTACCAA	ATATTTGCCA	TTGGATAAGG	GTATTAAACC	2700

TTATTATCCA GAACATCTAG TTAATCATTA CTTCCAAACC AGACATTATT TACACACTCT	2760
ATGGAAGGCG GGTGTATTAT ATAAGAGAGA AACTACACAT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCC TGGGAACAAG AGCTACAGCA TGGGGCAGAA TCTTTCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACT GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACTCCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTCTGGGCT GGGATTACAC CCACCGCACG GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACAAACCTTG CCAGCAAATC CGCCTCCTGC CTCCACCAAT CGCCAGTCAG	3120
GAAGGCAACC TACCCCTCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

AACTCCACAA CCTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT GTATTTCCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCCGA CTACTGTCTC TCCCATATCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGCG CTGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC TACCGTGTGT	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAACT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GATCTTCAAC TACCAGCAGG GGACCATGCA GAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTATCC CTCCTGTTGC TGTACCAAAC CTTCGGACGG AAATTGCACC	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGCATC	780
TTGAGTCCCT TTTTACCGCT GTTACCAATT TTCTTCTGTC TTTGGGTATA CATTTAAACC	840
CTAACAAAAC AAAAAGATGG GGTACTCTT TACATTTTAT GGGCTATGTC ATTGGATGTT	900

ATGGGTCATT GCCACAAGAT CACATCATAC AGAAAATCAA AGAATGCTTT AGAAAAC TTC	960
CTGTTAACAG GCCTATTGAT TGGAAAGTCT GTCAACGTAT TGTGGGTCTT TTGGGTTTTG	1020
CTGCCCCCTT TACACAATGT GGTATCCTG CTTTAATGCC TTTGTATGCA TGTATTCAGT	1080
CGAAGCAGGC TTTTACTTTC TCGCCAACTT ACAAGGCCTT TCTGTGTAAA CAATACCTGA	1140
ACCTTTACCC CGTTGCCCCG CAACGGCCAG GTCTGTGCCA AGTGTGCTT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGTC ATGGGCCATC AGCGCATGCG TGGAACCTTT CTGGCTCGTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCAGG TCTGGAGCAA	1320
ACATTCTCGG GACGGATAAC TCTGTTGTTC TCTCCCGCAA ATATACATCG TATCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTGTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCTTCTCGGG GTCGCTTGGG ACTCTCTCGT CCCCTTCTCC	1500
GTCTGCCGTT TCGACCGACC ACGGGGCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAAAGCC CAACCATTTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCTGT	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGAT TAAAGGTCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCTTG TTCATGTCTT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGATCCTTAT	1920
AAAGAATTTG GAGCTACTGT GGAGTTACTC TCGTTTTTGC CTTCTGACTT CTTTCCTTCA	1980
GTACGAGATC TTCTAGATAA CGCCTCAGCT CTGTATCGGG AAGCCTTAGA GTCTCCTGAG	2040
CATTGTTTAC CTCACCATAC TGCACTCAGG CAAGCAATAC TGTGCTGGGG GGAAC TAATG	2100
ACTCTAGCTA CCTGGGTGGG TGGTAATTTG GAAGATCCAA TATCCAGGGA CCTAGTAGTC	2160
AGTTATGTCA AACTAATAT GGGCCTAAAA TTCAGGCAAC TATTGTGGTT TCACATTTCT	2220
TGTCTCACTT TTGGAAGAGA AACAGTTATA GAGTATTTGG TGTCTTTTGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAGACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACGGG GCTTTATTCT TCTACTGTAC CTGTCTTTAA	2520
CCCTCATTGG AAAACACCCT CTTTTCCTAA TATACATTTA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAA TTTGTAGGCC CACTCACAGT CAATGAGAAA AGAAGACTGC AATTGATTAT	2640
GCCAGCTAGG TTTTATCCAA ATGTTACCAA ATATTTGCCA TTGGATAAGG GTATTAAACC	2700
TTATTATCCA GAATATTTAG TTAATCATTA CTTCCAACT AGACATTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ACAAGAGAGA AACTACACAT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGGCAGAA TCTTTCACC AGCAATCCTC	2880



TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTGGGGCT GGGATTCACC CCACCACACG GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT AGAAACGTTG CCAGCAAATC CGCCTCCTGC CTCTACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCGCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3182 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

AACTCCACAA CTTTCCACCA AACTCTGCAA GATCCCAGGG TGAGAGGCCT GTATTTCCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCCGA CTA CTGCCTC TCCCATATCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGCA CTGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAAC CACCGTGTGT	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAAT	360
TGTCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTCCTCTT CATCCTGCTT	420
CTATGCCTCA TCTTCTTGT GGTCTACTG GACTATCAAG GTATGTTGCC CGTGTGTCCT	480
CTAATTCAG GATCTTCAAC CACCAGCGCG GGACCATGCA GAACCTGCAC GACTACTGCT	540
CAAGGAACCT CTATGTATCC CTCCTGTTGC TGTACCAAAC CTTCGGACGG AAATTGCACC	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCA GTTTCGTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAATTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGCATC	780
TTGAGTCCCT TTTTACCGCT GTTACCAATT TTCTTTTGT TTTGGGTATA CATTTAAACC	840
CTAACAAAAC TAAGAGATGG GGTACTCTT TACATTTTCA TGGCTATGTC ATTGGAAGTT	900
ATGGGTCATT GCCACAAGAT CACATCATAC AGAAAATCAA AGAATGTTTT AGAAAACCTC	960
CTATTAACAG GCCTATTGAT TGGAAAGTCT GTCAACGTAT TGTGGGTCTT TTGGGTTTTG	1020

CTGCCCCTTT TACACAATGT GGTATCCTG CTTTAATGCC CTTGTATGCC TGTATTCAAT	1080
CTAAACAGGC TTTCACCTTC TCGCCAACTT ACAAGGCCTT TCTGTGTAAA CAATACCTGA	1140
ACCTTTACCC CGTTGCTAGG CAACGGCCAG GTCTGTGCCA AGTGTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGTC ATGGGCCATC AGCGCATGCG TGGAACCTTT CTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCAGG TCTGGAGCAA	1320
ACATTCTCGG GACGGATAAC TCTGTTGTTT TCTCCCGCAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCTTCTCGGG GCCGCTTGGG GATCTTTCGT CCCCTTCTCC	1500
GTCTGCCGTT CCGTCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCACTTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTTAAGG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGAT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTTAC CTCTGCCTAA TCATCTCTTG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTACTGT GGAGTTACTC TCATTTTTGC CTTCTGACTT TTTTCCTTCG	1980
GTACGAGATC TTCTAGATAC CGCCTCAGCT CTGTATCGGG ATGCCTTAGA GTCTCCTGAG	2040
CATTGTTTAC CTCACCATAC TGCACTCAGG CAAGCAATTC TTTGCTGGGG GGAACATAATG	2100
ACTCTAGCTA CCTGGGTGGG TGTTAATTTG GAAGATCCAG CATCTAGGGA CCTAGTAGTC	2160
AGTTATGTCA AACTAATAT GGGCCTAAAG TTCAGGCAAC TATTGTGGTT TCACATTTCT	2220
TGTCTCACTT TTGGAAGAGA AACAGTCATA GAGTATTTGG TGTCTTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGATCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAAGTGGGTA ACTTTACGGG GCTTTATTCC TCTACTGTAC CTGTCTTTAA	2520
CCCTCATTTG AAAACACCCT CTTTTCTTAA TATACATCTA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAA TTTGTAGGCC CACTCACAGT AAATGAGAAA CGAAGACTGC AATTAATTAT	2640
GCCTGCTAGG TTTTATCCAA ATGTTACTAA ATATTGCCA TTAGATAAGG GTATTAAACC	2700
TTATTATCCG GAACATTTAG TTAATCATT CTTCCAAACC AGACATTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGGGA AACAACAGT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGGCAGAA TCTTTCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000

CATTCGGGCT GGGATTACCC CCACCGCAGC GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATAAT ACAAACCTTG CCAGCAAATC CGCCTCCTGC ATCTACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCGCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

AACTCCACAA CATTTTCATCA AGCTCTGCAG GATCCCAGAG TAAGAGGCCT GTATTTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTGAAC CCTGTTCCGA CTACTGCCTC ACTCATCTCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGCA CCGAACATGG AAAGCATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC TCCCGTGTGT	300
CTTGGCCAAA ATTGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GATCATCAAC CACCAGCACG GGACCCTGCC GAACCTGCAT GACTCTTGCT	540
CAAGGAACCT CTATGTTTCC CTCATGTTGC TGTTCAAAAC CTTCGGACGG AAATTGCACT	600
TGTATTCCCA TCCCATCATC ATGGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCACT GGTTCGCCGG GCTTTCCCCC	720
ACTGTCTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACGACATC	780
TTGAGTCCCT TTATACCTCT GTTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAATC	840
CCAACAAAAC AAAAAGATGG GGATATTCCC TAAATTTTCAAT GGGTTATGTA ATTGGAAGTT	900
GGGGGTCATT ACCACAGGAA CACATCATAC AAAAAATCAA ACACTGTTTT GGAAACTCC	960
CTGTAAACCG GCCTATTGAT TGGAAAGTAT GTCAAGGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCTTT TACACAATGT GGGTATCCTG CTTTAATGCC TCTGTATACG TGTATTCAAT	1080
CTAAGCAGGC TTTCACTTTC TCGCCAACTT ACAAGGCCTT TCTGTGTAAA CAATACCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGCCAG GTCTGTGCCA AGTGTTTGCT GATGCAACCC	1200

CCACTGGCTG	GGGCTTGGCC	ATAGGCATTC	AGCGCATGCG	CGGAACCTTT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTTTTGC	TCGCAGCAGG	TCTGGAGCAA	1320
AACTTATCGG	GACCGATAAT	TCTGTCGTTC	TCTCCCGGAA	ATATACATCC	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GAGGGACGTC	CTTGCTCTAC	GTCCCGTCAG	1440
CGCTGAATCC	TGCGGACGAC	CCGTCTCGGG	GTCGCTTGGG	GATCTTTCGT	CCCCTTCTCC	1500
GTCTGCGGTT	CCGGCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CACCAAATCT	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCTCTGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	TTGTTTAAAG	ACTGGGAGGA	1740
GTTGGGGGAG	GAGATTAGAT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTTTAC	CTCTGCCTAA	TCATCTCTTG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTGGG	GCATGGACAT	TGACCCTTAT	1920
AAAGAATTTG	GAGCTACTGT	GGAGTTACTC	TCGTTTTTGC	CTTCTGACTT	CTTTCCTTCA	1980
GTAAGAGATC	TTCTAGATAC	CGCCTCAGCT	CTGTATCGGG	ATGCCTTAGA	ATCTCCTGAA	2040
CATTGTTTAC	CGCACCACAC	TGCACTCAGG	CAAGCCATTC	TTTGCTGGGG	GGAACATAATG	2100
ACTCTAGCTA	CCTGGGTGGG	TGTAAATTTG	GAAGATCCAG	CATCCAGGGA	CCTAGTAGTC	2160
AGTTATGTCA	ATACTAATAT	GGGCCTAAAG	TTCAGGCAAT	TATTGTGGTT	TCACATTTCT	2220
TGTCTCACTT	TTGGAAGAGA	AACCGTCATA	GAGTATTTGG	TGTCTTTTGG	AGTGTGGATT	2280
CGCACTCCTC	CAGCTTATAG	ACCACCAAAT	GCCCCTATCT	TATCAACACT	TCCGGAGAAT	2340
ACTGTTGTTA	GACGAAGAGG	CAGGTCCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGATCTCAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCCAG	CTTCCCAATG	TTAGTATTCC	2460
TTGGACTCAT	AAGGTGGGAA	ATTTTACGGG	GCTCTACTCT	TCTACTATTG	CTGTCTTTAA	2520
TCCTAACTGG	AAAACCTCAT	CTTTTCCTGA	TATTCATTG	CACCAGGACA	TTATTAACAA	2580
ATGTGAACAA	TTTGTAGGTC	CTCTAACAGT	AAATGAAAAA	CGAAGATTAA	ACTTAGTCAT	2640
GCCTGCTAGA	TTTTTTCCCA	TCTCTACAAA	ATATTTGCCC	CTAGAGAAAG	GTATAAAACC	2700
TTATTATCCA	GATAATGTAG	TTAATCATTG	CTTCCAAACC	AGACACTATT	TACATACCCT	2760
ATGGAAGGCT	GGGCATCTAT	ATAAAAGAGA	AACTACACGT	AGCGCCTCAT	TTTGTGGGTC	2820
ACCATATTCT	TGGGAACAAG	AGCTACATCA	TGGGGCTTTC	TTGGACGGTC	CCTCTCGAAT	2880
GGGGGAAGAA	TATTTCCACC	ACCAATCCTC	TGGGATTTTT	TCCCGACCAC	CAGTTGGATC	2940
CAGCATTCAG	AGCAAACACC	AGAAATCCAG	ATTGGGACCA	CAATCCCAAC	AAAGACCACT	3000
GGACGGAAGC	CAACAAGGTA	GGAGTGGGAG	CCTTCGGGCC	GGGGTTCACT	CCCCACACG	3060
GAGGCCTTTT	GGGGTGGAGC	CCTCAGGCTC	AAGGCATGCT	AAAAACATTG	CCAGCAGACC	3120
CGCCTCCTGC	CTCCACCAAT	CGGCAGTCAG	GAAGGCAGCC	TACCCCAATC	ACTCCACCTT	3180

TGAGAGACAC TCATCCTCAG GCCATGCAGT GG

3212

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AATTCCACAA CATTCCACCA AGCTCTGCAG GATCCCAGAG TAAGAGGCCT GTATTTTCCT	60
GCTGGTGGCT CCAGTTCGG AACAGTGAAC CCTGTTCCGA CTACTGCCTC ACTCATCTCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGCA CCGAACATGG AAAGCATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC TCCCGTGTGT	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC AGTCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GATCATCAAC CACCAGTACG GGACCCTGCC GAACCTGCAC GACTCTTGCT	540
CAAGGAACCT CTATGTTTCC CTCATGTTGC TGTTCAAAAC CTTCGGACGG AAATTGCACT	600
TGTATTCCCA TCCCATCATC ATGGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTTCTG GGTTCGCCGG GCTTTCCCCC	720
ACTGTCTGGC TTTTCTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATACCGCT GTTACCAATT TTCTTTTGTC TTTGGGTATA CATTTAAATC	840
CCAACAAAAC AAAAAGATGG GGCTATTCCC TTAATTTTCT GGGTTATGTA ATTGGAAGTT	900
GGGGCTCATT ACCACAGGAA CACATCATAC AAAAAATCAA AGACTGTTTT AGAAAACTCC	960
CTGTTAACCG GCCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCCTT TACACAATGT GGATATCTTG CTTTAATGCC TCTGTATGCA TGTACTCAAT	1080
CTAAGCAGGC TTTCACCTTC TCGCCAACCT ACAAGGCCTT TCTGTGTAAA CAATACCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGCCAG GTCTGTGCCA AGTGTTTGCT GATGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATAGGCATTC AGCGCATGCG CGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTTGC TCGCAGCAGG TCTGGAGCAA	1320

AACTTATCGG	GACCGATAAT	TCTGTCGTTT	TCTCCCGGAA	GTATACATCC	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GAGGGACGTC	CTTTGTCTAC	GTCCCGTCAG	1440
CGCTGAATCC	TGCGGACGAC	CCGTCTCGGG	GTCGCTTGGG	GATCTATCGT	CCCCTTCTCC	1500
GTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGTCTCC	CCGTCTGTTC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CACCAAATAT	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCTCTGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	TTGTTTAAAG	ACTGGGAGGA	1740
GTCGGGGGAG	GAGATTAGAT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTTCAC	CTCTGCCTAA	TCATCTCTTG	TTCATGTCTT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTTGGG	GCATGGACAT	TGACCCTTAT	1920
AAAGAATTTG	GAGCTACTGT	GGAGTTACTC	TCGTTTTTGC	CTTCTGACTT	CTTTCCTTCA	1980
GTAAGAGATC	TTCTAGATAC	CGCCTCAGCT	CTGTATCGGG	ATGCCTTAGA	GTCTCCTGAG	2040
CATTGTTTAC	CTCACCACAC	TGCACTCAGG	CAAGCCATTC	TTTGCTGGGG	AGAACTAATG	2100
ACTCTAGCTA	CCTGGGTGGG	TGTAAATTTG	GAAGATCCAG	CATCCAGGGA	CCTAGTAGTC	2160
AGTTATGTCA	ATACTAATAT	GGGCCTAAAG	TTCAGGCAAT	TATTGTGGTT	TCACATTTCT	2220
TGTCTCACTT	TTGGAAGAGA	AACCGTCATA	GAGTATTTGG	TGTCTTTTGG	AGTGTGGATT	2280
CGCACTCCTC	CAGCTTATAG	ACCACCAAAT	GCCCCATCTT	TATCAACACT	TCCGGAGAAT	2340
ACTGTTGTTA	GACGAAGAGG	CAGGTCCCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGATCTCAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCCAG	CTTCCCAATG	TTAGTATTCC	2460
TTGGACTCAT	AAGGTGGGAA	ATTTTACGGG	GCTTTACTCT	TCTACTATAC	CTGTCTTTAA	2520
TCCTAACTGG	AAAACCTCCAT	CTTTTCCTGA	TATTCATTTG	CACCAGGACA	TTATTAACAA	2580
ATGTGAACAA	TTTGTAGGTC	CTCTAACTGT	AAATGAAAAA	CGAAGATTAA	ACTTAGTCAT	2640
GCCTGCTAGA	TTTTTTTCCCA	TCTCTACGAA	ATATTTGCCC	CTAGAGAAAG	GTATAAAACC	2700
TTATTATCCA	GATAATGTAG	TTAATCATT	CTTCCAAACC	AGACACTATT	TACATACCCT	2760
ATGGAAGGCG	GGCATCTTAT	ATAAAAGAGA	AACTACACGT	AGCGCCTCAT	TTTGTGGGTC	2820
ACCTTATTCT	TGGGAACAAG	AGCTACATCA	TGGGGCTTTC	TTGGACGGTC	CCTCTCGAAT	2880
GGGGGAAGAA	TATTTCCACC	ACCAATCCTC	TGGGATTTTT	TCCCACCAC	CAGTTGGATC	2940
CAGCATTTCAG	AGCAAACACC	AGAAATCCAG	ATTGGGACCA	CAATCCCAAC	AAAGACCACT	3000
GGACAGAAGC	CAACAAGGTA	GGAGTGGGAG	CATTCGGGCC	TGGGTTCACT	CCCCCACACG	3060
GAGGCCTTTT	GGGGTGGAGC	CCTCAGGCTC	AAGGCATGCT	AAAAACATTG	CCAGCAGATC	3120
CGCCTCCTGC	CTCCACCAAT	CGGCAGTCAG	GAAGGCAGCC	TACCCCAATC	ACTCCACCTT	3180
TGAGAGACAC	TCATCCTCAG	GCCATGCAGT	GG			3212

(2) INFORMATION FOR SEQ ID NO: 311:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

AACTCAACTC ACTTCCACCA AGCTCTGTTG GATCCCAGGG TAAGGGCACT GTATTTTCCT	60
GCTGGTGGCT CCAGTTCAGG AACACAGAAC CCTGCTCCGA CTATTGCCTC TCTCACATCA	120
TCAATCTCCT CGAAGACTGG GGGCCCTGCT ATGAACATGG AGAACATCAC ATCAGGACTC	180
CTAGGACCCC TGCGCGTGTT ACAGGCGGTG TGTTCCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGACT ACCCAGGTGT	300
CCTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTTAC CAACCTCCTG TCCTCCAAC	360
TGTCCTGGCT ATCGTTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GACTACCAAG GTATGTTGCC CGTTTGTCCT	480
CTACTTCCAG GATCCACGAC CACCAGCAGG GGACCATGCA AAACCTGCAC AGCTCTTGCT	540
CAAGGAACCT CTATGTTTCC CTCCTGTTGC TGTTCCAAAC CCTCGGACGG AAACCTGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTA GGAAAATACC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCAA TTTGTTTCACT GGTGCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTTAGTTAT ATGGATGATC TGGTATTGGG GGCCAAATCT GTGCAGCATC	780
TTGAGTCCCT TTATACCGCT GTTACCAATT TTCTGTTATC TGTGGGTATC CATTTAAATA	840
CTGCTAAAAC AAAAAGATGG GGTTACAACC TACATTTTCA GGGTTATGTT ATTGGTAGTT	900
GGGGAACGTT ACCCCAAGAT CATATTGTAC ACAAATCAA AGATTGTTTT CGAAAAGTTC	960
CTGTAAATCG CCCAATTGAT TGGAAAGTTT GTCAAAGTAT TGTGGGTCTT TTGGGCTTTG	1020
CGGCCCCCTT TACCCAATGT GGTATCCTG CTCTCATGCC TTTGTATGCC TGTATTACTG	1080
CTAAACAGGC TTTTGTCTTC TCGCCAACTT ACAAGGCCTT TCTGTGTAAA CAATACATGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCAG GCCTGTGCCA AGTGTTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTTGCAG CTTGCTTCGC TCGCAGCCGG TCTGGAGCAA	1320
TCCTCATCGG CACAGACAAT TCTGTCGTCC TCTCTCGGAA GTATACATCC TTTCCATGGC	1380
TGCTCGGTTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC AGCGGACGAA CCCTCCCGGG GTCGCTTGGG GCTGTACCGC CCCCTTCTTC	1500

GTCTGCCGTT CCAGCCGACA ACGGGTCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTTC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CCCTGGAGTT TGCCAACAGT CTTACATAAG AGGACTCTTG GACTTTCAGG	1680
ACGGTCAATG ACCTGGATCG AAGACTACAT CAAAGACTGT GTATTTAAGG ACTGGGAGGA	1740
GCTGGGGGAG GAGATCAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTACCA GCACCATGCA ACTTTTTTAC CTCTGCCTAA TCATCTCTTG TTCATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTTCTGT GGAATTGTTT TCTTTTTTGG CTTCTGACTT CTTTCCGTCT	1980
GTTGGGGACC TCCTCGACAC CGCCTCAGCC CTGTACCGGG ATGCCTTAGA GTCACCGGAA	2040
CATTGCACCC CCAATCATAC CGCTCTCAGG CAAGCTATTT TGTGCTGGGG TGAGTTAATG	2100
ACTTTGGCTT CCTGGGTGGG TAATAATTTG GAAGACCCTG CAGCTAGGGA TTTAGTAGTT	2160
AATTATGTCA AACTAATAT GGGCTTAAAG ATTAGACAAC TATTGTGGTT TCACATCTCC	2220
TGTCTTACTT TTGGAAGAGA AACAGTTCTT GAGTATTTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCAC CTGCTTATAG ACCACCAAAT GCCCCTATCC TATCCACACT TCCGGAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCCT AGAAGAAGAA CTCCCTCGCC TCGCCGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCCAG CTCCCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGAA ATTTTACGGG GCTCTACTCT TCTACTGTAC CTGCTTTCAA	2520
TCCTAACTGG TTAACCTCTT CTTTCTCTGA TATTCATTTA CATCAGGATA TGATATCTAA	2580
ATGTGAACAA TTTGTAGGCC CGCTCACTAA AAATGAATTG AGAAGATTAA AATTGGTCAT	2640
GCCAGCTAGA TTTTATCCTA AGCATACCAA ATATTTCTTA TTGGAGAAAG GGATTAAACC	2700
CTATTATCCA GATCAGGCAG TTAATCATT A TTTTCAAACC AGACATTATT TGCATACTTT	2760
ATGGAAGGCG GGAATTCTAT ATAAGAGAGA AACCACACGT AGCGCCTCAT TTTGTGGGTC	2820
ACAAATATTCC TGGGAACAAG AGCTACAGCA TGGGAGCACC TCTCTCAACG ACAAGAAGGG	2880
GCATGGGACA GAATCTTTCT GTGCCCAATC CACTGGGCTT CTGCCAGAC CATCAGCTGG	2940
ATCCGCTATT CAGAGCAAAT TCCAGCAGTC CCGACTGGGA CTTCAACACA AACAAGGACA	3000
GTTGGCCAAT GGCAAACAAG GTAGGAGTGG GAGGCTACGG TCCAGGGTTC ACACCCCCAC	3060
ACGGTGGCCT GCTGGGGTGG AGCCCTCAGG CACAGGGTGT TTTAACAACC TTGCCAGCAG	3120
ATCCGCCTCC TGCTTCCACC AATCGGCTGT CCGGGAGGAA GCCAACCCAA GTCTCTCCAC	3180
CTCTAAGAGA CACACATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

AACTCAACTC ACTTCCACCA GGCTCTGTTG GATCCGAGGG TAAGGGCACT GTATTTTCCT	60
GCTGGTGGCT CCAGTTCAGG CACGCAGAAC CCTGCTCCGA CTATTGCCTC TCTCACATCA	120
TCAATCTCCT CGAAGACTGG GGGCCCTGCT ATGAACATGG ACAACATCAC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGTG TGTTCCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGACT ACCCGGGTGT	300
CCTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTTAC CAACCTCCTG TCCTCCAACT	360
TGTCCTGGCT ATCGTTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTAATTCCAG GATCTACGAC CACCAGCACG GGACCATGCA AAACCTGCAC AACTCTTGCT	540
CAAGGAACCT CTATGTTTCC CTCCTGTTGC TGTTCCAAAC CCTCGGACGG AAATGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTA GGAAATACC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCAA TTTGTTCAGT GGTGCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTTAGTTAT ATGGATGATC TGGTATTGGG AGCCAAATCT GTGCAGCATC	780
TTGAGTCCCT TTATACCGCT GTTACCAATT TTCTGTTATC TGTGGGTATC CATTTGAATA	840
CCTCTAAAAC AAAAAGATGG GGTTACAATT TACATTTTCAT GGGTTATGTC ATTGGCAGTT	900
GGGGAGCATT ACCCCAAGAT CATATTGTAC ACAAATCAA AGAATGTTTT CGAAAAGTTC	960
CTGTAAATCG TCCAATTGAC TGGAAAGTTT GTCAACGTAT TGTGGGACTT TTGGGCTTTG	1020
CTGCTCCTTT TACCCAATGT GGTTATCCTG CTCTCATGCC TCTGTATAAC TGTATCACTG	1080
CGAAACAGGC TTTTGTCTTT TCGCCAACTT ACAAGGCCCTT TCTCTGTAAC CAGTACATGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCAG GCCTGTGCCA AGTGTTTGCT GACGCAACCC	1200
CCACTGGTTG GGGCTTGGCC ATTGGCCATC AGCGCATGCG TGGAAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTTGCAG CTTGCTTCGC TCGCAGCCGG TCTGGAGCAA	1320
TCCTCATCGG CACAGACAAT TCTGTCTGCC TCTCCCGGAA GTATACATCC TTTCCATGGC	1380
TGCTCGGATG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC AGCGGACGAA CCCTCCCGGG GCCGCTTGGG GCTCTACCGC CCTCTTCTGC	1500
GTCTGCCGTT CCAGCCGACC ACGGGTCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTTC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620

CGTGAACGCC CCCTGGAGTT TGCCAACAGT CTTACATAAG AGGACTATTG GACTTTCAGG	1680
ACGGTCAATG ACCTGGATCG AAGAATACAT CAAAGACTGT GTATTTAAAG ACTGGGAGGA	1740
GCTGGGGGAG GAGATCAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTCTTG TTTATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTTGGG GCATGGACAT TGACCCCTTAT	1920
AAAGAATTTG GAGCTTCTGT GGAATTGTTT TCTTTTTTGC CTTCTGACTT CTTTCCGTCA	1980
ATCCGAGACC TTCTCGACAC CGCCTCAGCT CTGTATCGGG ATGCGTTAGA GTCACCGGAA	2040
CATTGCACCC CCAATCATAC CGCTCTCAGG CAAGCTATTT TGTGTTGGGG TGAATTAATG	2100
ACTTTGGCTT CCTGGGTGGG CAATAATTG GAGGACCCTG CAGCCAGGGA TTTAGTAGTT	2160
AACTATGTTA AACTAATAT GGGCTTAAAG ATTAGACAAC TATTGTGGTT TCACATTTCC	2220
TGCCTTACTT TTGGAAGAGA AACAGTTCTT GAGTATTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCC TATCCACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCCAG CTTCCCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGAA ATTTTACGGG GCTCTACTCT TCTACTGTAC CTGCTTTCAA	2520
TCCTCACTGG TTAACCTCTT CTTTTCCTGA TATTCATTTG CATCAAGACC TGATATCTAA	2580
ATGTGAACAA TTTGTAGGCC CACTTACCAA AAATGAATTG AGAAGGTTGA AATTGATTAT	2640
GCCAGCCAGA TTCTTTCCTA AACTTACTAA ATATTTCCCT CTGGAGAAAAG ACATTAAACC	2700
TTATTATCCA GAGCATGCAG TTAATCATT TTTTCAAACC AGACATTATT TGCATACTTT	2760
ATGGAAGGCG GGAATTTTAT ATAAGAGAGA ATCCACACGT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGCACC TCTCTCAACG ACAAGAAGGG	2880
GCATGGGACA GAATCTCTCT GTGCCCAATC CACTGGGATT CTTTCCAGAC CATCAACTGG	2940
ATCCTCTTTT CAGAGCAAAT TCCAGCAGTC CCGATTGGGA CTTCACAAA AACAAGGACA	3000
CTTGGCCAAT GGCAAACAAG GTAGGAGTGG GAGGTTACGG TCCAGGGTTC ACACCCCCAC	3060
ACGGTGGCCT GTTGGGGTGG AGCCCTCAGG CACAAGGTGT TCTAACAACC TTGCCAGCAG	3120
ATCCGCCTCC TGCCTCCACC AATCGGCTGT CCGGGAGGAA GCCAACCCCA GTCTCTCCAC	3180
CTCTAAGAGA CACACATCCA CAGGCAATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AACTCAACCC AGTTCACCA AGCTCTGTTG GATCCCAGGG TAAGGGCTCT GTACTTCCCT	60
GCTGGTGGCT CCAGTTCAGG GACACAGAAC CCTGCTCCGA CTATTGCCTC TCTCACATCA	120
TCAATCTTCT CGAAGACTGG GGGCCCTGCT ATGAACATGG ACAACATTAC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGTT ACAGGCGGTG TGTTCCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGACT ACCCGGGTGT	300
CCTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTTAC CAACCTCCTG TCCTCCAAC	360
TGTCCTGGCT ATCGTTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTT GGTTCCTCTG GACTATCAAG GTATGTTGCC CGTTTGTCTT	480
CTACTTCCAG GATCCACGAC CACCAGCACG GGACCCTGCA AAACCTGCAC AACTCTTGCA	540
CAAGGAACCT CTATGTTTCC CTCCTGTTGC TGTTCCAAAC CCTCGGACGG AAACCTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTA GGAAAATACC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCAA TTTGTTTCACT GGTGCGTCGG GCTTTCCCCC	720
ACTGTTTGGC TTTTAGTTAT ATGGATGATC TGGTATTGGG GGCCAAATCT GTGCAGCATC	780
TTGAGTCCCT TTATACCGCT GTTACCAATT TTCTGTTATC TGTGGGTATC CATTTAAATA	840
CCTCTAAAC AAAAAGATGG GGTTACTCCC TACATTTTAT GGGTTATGTC ATTGGTAGTT	900
GGGGATCATT ACCCAAGAT CACATTGTAC ACAAATCAA GGAATGCTTT CGAAAACGTC	960
CTGTAAATCG TCCAATTGAT TGGAAGTTT GTCAACGCAT AGTGGGTCTT TTGGGCTTTG	1020
CTGCCCCTTT CACCAATGC GGTATCTCTG CTCTCATGCC TCTGTATGCC TGTATTACTG	1080
CTAAACAGGC TTTTGTCTTC TCGCCAACCT ACAAGGCCTT TCTGTGTAAA CAATACATGA	1140
ACCTTTACCC GGTGCTCGG CAACGGCCAG GCCTGTGCCA AGTGTGCTT GACGCAACCC	1200
CCACTGGTTG GGGCTTGGCC ATTGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTCGC TCGCAGCAGG TCTGGAGCGA	1320
CTCTCATCGG CACGGACAAT TCTGTTGTCC TCTCTAGGAA GTACACCTCC TTTCCATGGC	1380
TGCTCGGATG TGCTGCAAAC TGGATCCTGC GCGGGACGTC CTTTGTGTTAC GTCCCATCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCCCGGG GCGGCTTGGG GCTGTACCGC CCTCTTCTCC	1500
GTCTGCCGTT CCAGCCGACG ACGGGTCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTTC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CCCTGGAGTT TGCCAACAGT CTTACATAAG CGGACTCTTG GACTTTCAGG	1680
ATGGTCAATG ACCTGGATCG AAGAATACAT CAAAGACTGT GTATTTAAGG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGGT TAAAGGTCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800

CTGTTACCA GCACCATGCA ACTTTTTCAC CTCTGCCTAA TCATCTTTTG TTCATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTTG GAGCTTCTGT GGAGTTACTC TCGTTTTTGC CTTCTGATTT CTTCCCATCG	1980
GTTCGGGACC TACTCGACAC CGCTTCAGCT CTTTACCGGG ATGCTTTAGA GTCACCTGAA	2040
CATTGCACTC CCAACCATAC TGCTCTCAGG CAAGCTATTT TGTGTTGGGG TGAGTTAATG	2100
ACTTTGGCTT CCTGGGTGGG CAATAATTTG GAGGACCTG CAGCTAGGGA TTTAGTAGTT	2160
AACTATGTTA AACTAACAT GGGCCTAAAA ATTAGACAAC TGTGTGGTT TCACATTTCC	2220
TGCCTTACTT TTGGAAGAGA AACAGTTCTA GAGTATTTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CTGCTTACAG ACCACCAAAT GCCCCTATCC TATCCACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGATCTCAAT CGCCGCGTCG CCGCAGATCT CAATCTCCAG CTTCCCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACGGG GCTTTACTCT TCTACTGTGC CTGCTTTTAA	2520
TCCTAACTGG TCCACTCCTT CTTTTCTGA TATTCATTG CATCAAGACC TGATTTCTAA	2580
ATGTGAACAA TTTGTAGGCC CACTTACTAA AAATGAATTA CGAAGATTAA AATTGGTTAT	2640
GCCAGCTAGA TTTTATCCTA AGGTTACCAA ATATTTTCCC ATGGATAAAG GCATCAAACC	2700
CTATTATCCT GAGCATGCAG TTAATCATTA CTTTAAAACC AGACATTATT TGCATACTTT	2760
ATGGAAGGCG GGAATTTTAT ATAAGAGAGA ATCCACACGT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCC TGGGAACAAG AGCTACAGCA TGGGAGCACC TCTCTCAACG ACACGAAGAG	2880
GCATGGGACA GAATCTCTCT GTGCCCAATC CTCTGGGATT CTTTCCAGAC CATCAGCTGG	2940
ATCCGCTATT CAGAGCAAAT TCCAGCAGTC CCGACTGGGA CTTCAACACA AACAAGGACA	3000
GTTGGCCAAT GGCAAACAAG GTAGGAGTGG GAGGCTACGG TCCAGGGTTC ACACCCCCAC	3060
ACGGTGGCCT GCTGGGGTGG AGCCCTCAAG CACAAGGTGT GTTAACAACC TTGCCAGCAG	3120
ATCCGCCTCC TGCTTCCACC AATCGGCGGT CCGGGAGAAA GCCAACCCCA GTCTCTCCAC	3180
CTCTAAGAGA CACACATCCA CAGGCAATGC AGTGG	3215